

	AGAATAATTG TGTATGAAG CTGCCTTATT TTTTTCCTT TTGTAAGTTA CTATTTTCAT	1920
	GTGAATATTT ATGTAGATAA AATTTGCCTC CTGGTAACCC TGTAATGGAT GGGGCCAG	1980
5	AATGAAATAT TTGAGAAAA CAAGTAAAA GGTCAAGATA CAAATGTGTA TTAAAAAAA	2040
	AAAAGCCTAT TAATAGGGTT TCTGCGCGGT GCAGGGTTGT AAACCTGCTT TATCTTTTAG	2100
10	GATTATTCCT AAATGCATCT TCTTTATAAA CTGACTTGC TATCTCAGCA AGATAAATTA	2160
	TATTAAAAAA ATAAGAATCC TGCAGTGTTC AAGGAACCTCT TTTTGTGTAA ATCACGGACA	2220
	CCTCAATTAG CAAGAACTGA GGGGAGGGCT TTTCCATTG TTTAATGTTC TGTGATTTT	2280
15	AGCTAAAGAG AGGGAACCTC ATCTAAGTAA CATTTCACAC TGGATACAGC AAAAGGAGTT	2340
	CATTGCAATA CTGTCTTTGG ATATTGTTC AGTACTGGGT GTTTAAAGGA CAAATAGCTG	2400
20	CTAGAATTCA GGGTAAATG TAAGTGTTC GAAAACGTCA GAACATTTGG GGTTTTAAAC	2460
	TGATTGTTC CTCCCTATCC AGCCTAGACA CCAGTAACTC TTGTGTTCAC CAGGACCCAG	2520
	ACCCTTGGCA AGGATAGGC TCGTTGGTGA CATTGTGAAT TTCAGATTTC TTTTATCCAC	2580
25	TTTTTTTGCT ATTTATTTAA ATGGTCGATC AACTTCCCAC AACTGAGGA ATGAATTCCA	2640
	CGAGCCTGTT CTGAAATGT GGACGTAAGA CAAACAGTG CTCGTCCTTT AATGGAGTTC	2700
30	ACCAGCACAC TTGTTAACCA GTCCTGTTTC CTTCGTCCT TTTTGTGCG TAATAAAGTC	2760
	AACTGACCAA GTGACCATGA AAAGGGGCTG TCTGGGGCTC CTGTTTTTTA GCTGCTGTTC	2820
	TTCAGCTCCG ACCATGTTGC TGTGTGATTA TCTCAATTGG TTTAATTTGA GGCAGAAACT	2880
35	GAAGCTCTAC CAATGAACTG TTTAGAAACA AGACACACTT TTGTATTAAA ATTGCTTGCA	2940
	GTAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCCC GGTAC	2995

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(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

	GGGACCCGCG CGSCTCCCGG GGATGGTGAG CAAGGCGCTG CTGCNWCCTG TCTGCCGTCA	60
	ACCGCAGAGG ATGAAGCTGC TGCTGGGCAT CGCCTTGCTG GCCTACGTCG CCTCTGTTTG	120
55	GGGCAACTTC GTTAATATGA GGTCTATCCA GGAAATGGT GAACTAAAAA TTGAAAGCAA	180
	GATTGAAGAG ATGTTTGAAC CACTAAGAGA GAAAATCAGA GATTTAGAAA AAAGCTTTAC	240
60	CCAGAAATAC CCACCACTAA AGTTTTTATC AGAAAAGGAT CGGAAAAGAA TTTTGAWTAA	300

	CAGGAGGGCG AGKGTTCGTG GGCTCCCATC TKAAC TGACA AACTCATGAT GGACGGCCAC	360
5	GAGGTGACCG TGGTGGACAA TTTCTTCACG GGCAGGAAGA GAAACGTGGA GCACTGGATC	420
	GGACATGAGA ACTTCGAGTT GATTAACCAC GACGTGTGGG AGCCCCCTCTA CATCGAGGTT	480
	GACCAGATAT ACCATCTGGC ATCTCCAGCC TCCCCTCCAA ACTACATGTA TAATCCTATC	540
10	AAGACATTAA AGACCAATAC GATTGGGACA TTAAACATGT TGGGGCTGGC AAAACGAGTC	600
	GGTGCCCGTC TGCTCCTGGC CTCCACATCG GAGGTGTATG GAGATCCTGA AGTCCACCCCT	660
15	CAAAGTGAGG ATTACTGGGG CCACGTGAAT CCAATAGGAC CTCGGGCGCTG CTACGATGAA	720
	GGCAAAACGTG TTGCAGAGAC CATGTGCTAT GCCTACATGA AGCAGGAAGG CGTGGGAAGTG	780
	CGAGTGGCCA GAATCTTCAA CACCTTTGGG CCACGCATGC ACATGAACGA TGGGCGAGTA	840
20	GTCAGCAACT TCATCCTGCA GGCCTCCAG GGGGAGCCAC TCACGGTATA CGGATCCGGG	900
	TCTCAGACAA GGGCGTTCCA GTACGTCAGC GATCTAGTGA ATGGCCTCGT GGCTCTCATG	960
25	AACAGCAACG TCAGCAGCCC GGTCAACCTG GGAACCCAG AAGAACACAC AATCCTAGAA	1020
	TTTGCTCAGT TAATTAAAA CCTTGTGGT AGCGGAAGTG AAATTCAGTT TCTCTCCGAA	1080
	GCCCAGGATG ACCCAGAGAA AAGAAAACCA GACATCAAAA AAGCAAAGCT GATGCTGGGG	1140
30	TGGGAGCCCG TGGTCCCGCT GGAGGAAGGT TTAAACAAAG CAATTCAC TA CTTCCGTAAA	1200
	GAACTCGAGT ACCAGGCAAA TAATCAGTAC ATCCCCAAAC CAAAGCCTGC CAGAATAAAG	1260
35	AAAGGACGGA CTCGCCACAG CTGAACTCCT CACTTTTAGG ACACAAGACT ACCATTGTAC	1320
	ACTTGATGGG ATGTATTTTT GGCTTTTTTT TGTGTGCGTT TAAAGAAAGA CTTTAACAGG	1380
	TGTCATGAAG AACAACTGG AATTTTCATTC TGAAGCTTGC TTAAATGAAA TGGATGTGCC	1440
40	TAAAGCTCC CCTCAAAAA CTGCAGATTT TGCCTTGAC TTTTGAATC TCTCTTTTTA	1500
	TGTAAATAG CGTAGATGCA TCTCTGCGTA TTTTCAAGTT TTTTATCTT GCTGTGAGAG	1560
45	CATATGTTGT GACTGTGCTT GACAGTTTAA TTTACTGGTT TCTTTGTGAA GCTGAAAAGG	1620
	AACATTAAGC GGGACAAAA ATGCCGATTT TATTTATAAA AGTGGTACT TAATAAATGA	1680
	GTCGTTATAC TATGCATAAA GAAAAAYCCT AGCAGTATTG TCAGGTGGTG GTGGCCCGGC	1740
50	ATTGATTTTA GGGCAGATAA AAGAATTCTG TGTGAGAGCT TTATGTTTCT CTTTTAATTC	1800
	AGAGTTTTC CAAGTCTAC TTTTGAGTTG CAAACTTGAC TTTGAAATAT TCCTGTTGGT	1860
55	CATGATCAAG GATATTTGAA ATCACTACTG TGTTTTGCTG CGTATCTGGG GCGGGGGCAG	1920
	GTTGGGGGGC ACAAAGTTAA CATATTCTTG GTTAACCATG GTTAAATATG CTATTTTAAT	1980
60	AAAATATTGA	1990

(2) INFORMATION FOR SEQ ID NO: 276:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

	AACTTCGCTT AGCTCTCCAG GGTNAAACGG GTGAGNCCTT AAAACAGAA GAGAACAAGA	60
15	TTTAAAGTCC GTTGCAATGA AAATAACAAA CAATATCAAT GTTTTAATCA AGGATCTCTT	120
	CCACATTCCT CCTTCTTATA AGAGCACAGT AACACTATCC TGGAAACCTG TACAAAAGGT	180
20	TGAGATTGGG CAAAAGAGAG CCAGTGAAGA TACAACCTCA GGTTCAACCAC CCAAGAAATC	240
	TTCAGCAGGA CCAAAAAGAG ATGCCAGGCA GATTTATAAC CCTCCAGTG GGAAATATAG	300
	CAGCAATTTG GGCAACTTTA ATTATGAGCA GAGAGGAGCC TTCAGGGGAA GTAGAGGTGG	360
25	CCGAGGTTGG GGCACACGAG GAAATCGTAG TCGGGGAAGA CTCTACTGAA TAAGACATCA	420
	GCATTCTTCA GCATGTTCAT GAGCTTAATA TACTTAAATT CTACTACTCA TTGGATTGCC	480
30	GGGGATGTCC CTTTAAACAG ACTGCTGCCT TCAGCTAAAA ACTTAATGTT CTTTATACCT	540
	TTGTATGTAT GACCTACTTT TGTAACAGAC CATGGTTGTG TCCAAGGTAA AACCACAGTG	600
	ATATTTTGGG ATGCTTTGTC TGCAATCTTG ACTTGTTTT GCAGTATCAT TATTCAGACT	660
35	TCAAATGTG AATCTTTTAA ACATCTTGAT AATTGTGTG TGAGAGCTGT TCATTCTAAA	720
	ATGTAATGAA ATTCAGTCTA GTTCTGCTGA TAAAGATCAT CAGTTTTGAA AGGTTACTGA	780
40	TTTTCCTCTT CCTCTTAGT TTTTACCCA ATATATGGAG AAGAGTAATG GTCAATCTTA	840
	ACATTTTGT TTAATGTGT AATAAGCTG CTGGGCAGTG GTGCAGCATT CCTACCTAGT	900
	GTCATAAAG CAAAATACTT ACATAGCTTT CTTAAAATAT AGGAATGACA TTACATTTTT	960
45	AGGAGAAAGT AAGTTGCTTT GCACCGCTTA CTTAATTCTT TTCCATATAT TGTGATACAA	1020
	ACTTTTGAAT ATGGAATCTT ACTATTTGAA TAGAAATGTG TATGTATAAT ATACATACAT	1080
50	ACATAAGCAT ATATGTGTGT GTGTGTGTGT ATATATATAT ATATGCATGC TGTGAACTT	1140
	GACTACACAA CATAAATCAC TTTTAAATT CCAGGAACGG GTAGTCTGAC ACGGTGATTA	1200
	TCCTTTTGAG GCTGAATCCG TTATTAACCT GTTATTTAGG TTTTACTCC CAGTAGCAAG	1260
55	GGATTCTAAG TTAGTTGCAC TTACATGATT ATTGTTATTT AAAACTAAGA ATAAAGGCTG	1320
	CATTTTCAAA GATAAATGG AATTGCTGTT GGTGAAATAA CAACCAAAT ACTGAATCTG	1380
60	ATGTACATAC AGGTTTCTAC AGGAAGAGAT GGTATAATTT ACAATTGGA GATTTAATAA	1440

	CCAGGGCTAC CCAGAAAAAG TGACTTGATA ACATGGTACC AATAAGTAAG GGATGCTCTC	1500
	TCGGTTTGCT TTTGCCACTT TCAAGATTTT AACTTCTCAG GTTATTAAATC AAAATTATTG	1560
5	TATAAGTTAG CCAATAGAAT TTTTAGGTTA AAACAACAGA TGGGGGGTTT GTGGAGTGT	1620
	TAATGTCATG GGCATTTTTA GTAGCATAGA CCCTTTGTTC TGCATTTGAA TGTTCGTAT	1680
10	ATTTTGTGTT CACAGTTAAT CTCCCTCCC CAAGTTTGCT ATTCAAATCA ACTGCCTGAA	1740
	TGACATTTCT AGTAGTCTGA TGTATTTTTC TGAGGAATAG TTTGTGATTC CAATGCAGGT	1800
	GTCTTCATTA CCATTACCTC TACACTGCAG AAGAAGCAAA ACTCCTTTAT TAGAATTACT	1860
15	GCACATGTGT ATGGGGAAAA TAGTTCTGAA AGGCTAGAAT GATACAAGTG AGCAAAAGTT	1920
	GGTCAGCTTG GCTATGGAGT GGTGGCAATA ATCTCTAAAC ATTCCAAAAG ACCATGAGCT	1980
20	GAACCTAAAC TCCCTTGAA TCTGAACAAA GGAATATAAA ATTGCCATTT GAAAACGAC	2040
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	2100
	AATTATAGAG ACTACAGCTA AATAAATTG AACATTAAAT ATAATTTTAC CACTTTTGT	2160
25	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	2220
	GATACTGAGT TGACTGTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	2280
30	GTGCACAACT TAGGTTATTT TTGCTTCCGA ATTGAATGA AAAACTTAAT GCCATGGATT	2340
	TTTTTCTTTT GCAAGACACC TGTATTATCAT CTGTTTTAA TGTAAATGTC CCCTTATGCT	2400
	TTTGAAATAA ATTTCCTTTT GTAATTTTAA AAAAAA	2436
35		

(2) INFORMATION FOR SEQ ID NO: 277:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 782 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
45	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:	
	GCCACTGACT TCTCCACCCC TTCTGTCTCC CCCATAATAG TTTATTTGGT TGGTCTGGAC	60
50	TCACCTGTGG CCTTTRATTA AATTCCCTAAG GGGCCTGAAG AAGACATTTT TACTGCAGAG	120
	GGTTAGAGGC ACTTGAGCAA GGCCCCACA TCCCAACTCT GGGAGTTGTG GTGGGAGGAG	180
55	GCACTTCTGG GGGATAGGAC CAGACAAGAT AACAGGAGCT CACATGGNAA GCAGAAGCTG	240
	TGACAAGTTT AGTAGTCCCA AAATGGGTTA TATCCCTTCC CCCTTTACAT CAGAATCTTG	300
	TGAAATGGGA AAACAACAGA AGGAGGGGAT CAAAGATAGC TGATCTCACA TGCTTCCCAG	360
60	GCAGGSCARA GGTGGGAGTC AAACCCGGGT GACAGGTGGG TGGAGAGCCC TGTTTGAGGT	420

TGTGGCTGAT CCCTCTCTGG TATTAGTTTT TCCCTGGGA GCAGGAAGCC CTAGGAAGAG 480
 5 GGGACTGCAG GGTCCTCRGG GGATCTTTCC TCCCTCCCT GCATGAGGCA GAGGCAAGCT 540
 GCCTGCCAAC CCCTCCCTC AAGGAATGGC CTGCCCAGG AATGCCACC ACACATACCC 600
 TCTTCTTTTT TTCTAGTCAA ACTCTGTGT ATTCTTGGC TTGCTCCCT CCTTCTCCC 660
 10 CTCTCAACCT TTACTTCTGA TTTCTATTTC ATGGAATTG GGATTGAAGT TAAACTACAA 720
 CAGTGCCTCC AACACCAAGT CTGTCAGGAA AAAAATACAA AGAAATTTAA CAAAAAATAA 780
 AA 782
 15

20 (2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 961 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

30 GAGTTCGGGC TGGAGACCCG TGCTCTGGGC CGGCGCCTTC ACCATGGCCT CGGCAGAGCT 60
 GGACTACACC ATCGAGATCC CGGATCAGCC CTGCTGGAGC CAGAAGAACA GCCCCAGCCC 120
 AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC TGTGGTGATT CTYTTGGGCT GGGGTGGCTG 180
 35 CAAGGACAAG AACCTTGCCA AGTACAGTGC CATCTACCAC AAAAGGGGCT GCATCGTAAT 240
 CCGATACACA GCCCCGTGGC ACATGGTCTT CTCTCCGAG TCACTGGGTA TCCCTTCACT 300
 TCGTGTTTGG GCCCAGAAGC TGCTCGAGCT GCTCTTTGAT TATGAGATTG AGAAGGAGCC 360
 40 CCTGCTCTTC CATGTCTTCA GCAACGGTGG CGTCATGCTG TACCGCTACG TGCTGGAGCT 420
 CCTGCAGACC CGTCGCTTCT GCGCGCTGCG TGTGGTGGGC ACCATCTTTG ACAGCGCTCC 480
 45 TGGTGACAGC AACCTGGTAG GGGCTCTGCG GGCCCTGGCA GCCATCCTGG AGCGCCGGGC 540
 CGCCATGCTG CGCTGTGTC TGCTGGTGGC CTTTGCCCTG GTGGTCTGTC TGTTCACGT 600
 CCTGCTTGCT CCCATCACAG CCTCTTTCCA CACCCACTTC TATGACAGGC TACAGGACGC 660
 50 GGGCTCTGCG TGGCCCGAGC TCTACCTCTA YTCGAGGGCT GACGAAGTAG TCCTGGCCAG 720
 AGACATAGAA CGCATGGTGG AGGCACGCTT GGCACGCCG GTCTTGGCGC GTTCTGTGGA 780
 55 TTTCGTGTCA TCTGCACACG TCAGCCACCT CCGTGACTAC CCTACTTACT ACACAAGCCT 840
 CTGTGTGAC TTCATGCGCA ACTGCGTCCG CTGCTGAGGC CATGTCTCCA TCTCMTCT 900
 60 GCTCCAGAAA TAAATGCCTG ACAMCTCCCC AAAAAAAAAA AAAAAAAAAA ACTCGAGGGG 960

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961

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CGCGCTTTGC AGTTCGGTCT CCTGGTGTAC GGCCAACGCC AAGTAGGGGA TTGCGTTCCC	60
TCCAGTCGCA GCCCTATCAG ATTGGATAT GTCTTCATA TTGATTGGA TTTACAGTGG	120
20 TTTACAGCAGT GTGCTACAGT TTTTAGGATT ATATAAGAAA ACTGGTAAAC TGGTATTTCT	180
TGGATTGGAT AATGCAGGAA AAACAACATT GCTACACATG CTAAAAGATG ACAGACTTGG	240
25 ACAACATGTC CCAACATTAC ATCCCACTTC CGAAGAATG ACCATTGCTG GCATGACGTT	300
TACAACTTT GATCTGGGTG GACATGTTCA AGCTCGAAGA GTGTGGAAAA ACTACCTTCC	360
TGCTATCAAT GGCATGTAT TTCTGGTGA TTGTGCAGAC CACGAAAGGC TGTTAGAGTC	420
30 AAAAGAAGAA CTTGATTAC TAATGACAGA TGAAACCATT GCTAATGTGC CTATACTGAT	480
TCTTGGGAAT AAGATCGACA GACCTGAAGC CATCAGTGAA GAGAGGTTGC GAGAGATGTT	540
TGGTTTATAT GGTGAGACAA CAGGAAAGGG GAGTATATCT CTGAAAGAAC TGAATGCCCG	600
35 ACCCTTAGAA GTTTTCATGT GTAGTGTGCT CAAAAGACAA GGTACGGAG AAGGCTTCCG	660
CTGGATGGCA CAGTACATTG ATTAACACAA ACTCACATG GTTCCAGGTC TCAACGTTCA	720
40 GGCTTACTCA GAGATTGAT TGCTCAACAT GCATAACTTG AATTCAATAG ACTTTTGCTG	780
GTTATAAAAC AGATGTTTTT TAGATTATTA ATATTAAATC AACTTAATTT GAATGAGAAT	840
TGAAACTGA TTCAAGTAAG TTTGAGTATC ACAATGTTAG CTTTCTAATT CCATAAAAGT	900
45 ACTTGGTTTT TACAGTTTAT AATCTGACAT CACCCAGCG CCATTGTAA AGAGCAACTT	960
TCCAGCAGTA CATTTGAAGC ACTTTTAAAC AACATGAAAC TATAAACCAT ATTTAAAAGC	1020
50 TCATCATGTT AAATTTTTTA TGTACTTTTC TGGAAGTAGT TTTTAAATTT TAGATTATAT	1080
GTCCACCTAT CKTAAGTGTA CAGTTAATAA TTAGCTTATT CAATGATTGC ATGATGCCTT	1140
ACAGTTTCA ATAACTTTTT TTCTTATGCA AACGTCATGC AATAAAACAA ACTCTAATGT	1200
55 TTGGCAAAAA AAAAAAAAAA AAANTCGA	1228

60

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

10 TCTCGGGTCT CGGACAGGT GAGCACCTG ATGAAGGCCA CGGTCTGAT GCGGCACCTG 60
 GCGGGGTGCA GGAGATCGTG GCGCCCTCC GCAAGGGCGS CGGAGACCGG TTACAGGTGA 120
 15 TTCTGATTT TRACATGACC TTGAGCAGGT TTGCATATAA TGGAAAGCGA TGCCCTTCTT 180
 CTTACAATAT TCTGGATAAT AGCAAGATCA TCAGTGAGGA GTGTGCGAAA GAGCTCACAG 240
 20 CGTCTCTTCA CCACTATTAC CCAATGAGA TCGACCCACA CCGGACCGTC AAGGAGAAGC 300
 TACCTCATAT GGTGGAATGG TGGACCAAAG CGCACAATCT CCTATGTCAG CAGAAGATTC 360
 AGAAGTTTCA GATAGCCCGAG GTGGTTAGAG AGTCCAATGC AATGCTCAGG GAGGGATATA 420
 25 AGACCTTCTT CAACACACTC TACCATAACA ACATTCCOCT TTTCATCTTT TCTGCGGGCA 480
 TTGGTGATAT CCTGGAAGAA ATTATCCGAC AGATGAAAGT GTTCCACCCC AACATCCACA 540
 30 TGTGTCTAA CTACATGGAT TTAAATGAAG ATGGTTTCTT CCAGGGATTT AAGGGCCAGC 600
 TGATACACAC ATACAACAAG AACAGCTCTG TGTGTGAGAA CTGTGGTTAC TTCCAGCAAC 660
 TTGAGGCAAA AACCAATGTC ATCCTGCTGG GAGACTCTAT CGGGGACCTC ACCATGGCCG 720
 35 ATGGGGTTCC TGGTGTGAG AACATTCTCA AAATGGCTT CCTGAATGAC AAGGTGGAGG 780
 AGCGGCGGGA NCGCTAACAT GGAATCCTAT GACATCGTGC TGGAGAAGGA CGAGACTCTG 840
 40 GATGTGGTCA ACGGGCTACT GCAGCACATC CTGTGCCNAG GGGGTCCAGC TGGAGATGCA 900
 AGGCCCCCTGA AGGCGCAGGC TCCNAAGKCC SCTGCAGGCC GTGGTGAGGA GGGGCGCCTC 960
 CCCAGAGTCT GCTCCCCCGT GAACACAGAG CAGAGCCAGG GTGGCCAGCA GTGGCTGGGT 1020
 45 CCTTCCGCGC CCTCCGTCC TCCTTTCCCT GAGCACCTTC ATCACCAGAG GCTTGAAGGA 1080
 ACCCCGCCAT GTGGCAGGGC ACAGGCACTG TTCTGGTGA ACCTTGGACC ACAGCATGTC 1140
 50 AGTGCTCTAG GGATTGTCTA CTCCAGGGAT TTTCTTCAAA ATTTTAAAC ATGGGAAGTT 1200
 CAAACAAATA TAATGTGTGA AACAGATCAA AATTTTAAA ATGAAAAAAA AGCTGCTCTG 1260
 ATTCAGGGGA TGTGGGTCGG GGTAGAACCT GGACCTCTTG GCTTGGGGC ACATGGGATG 1320
 55 CTTCTAG 1327

60 (2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

10 TCACCCCTGCC TACAGCGTGG AGCTCAGATG ACTGCGCCCT CCACGGTCAC TGTGAGCAGG 60
 TGGTATTCAC AGCCTGCATG ACCCTCACGG CCAGCCCTGG GGTGTTCCCC GTCAGTGTGT 120
 GGCTTTGGCT GAAGCCTAAT TCCACAGCTC CTTGTTTTTT GAGAGAGACT GAGAGAACCA 180
 15 TAATCCTTGC CTGCTGAACC CAGCCTGGGC CTGGATGCTC TGTGAATACA TTATCTTGCG 240
 ATGTGGGTT ATTCCAGCCA AAGACATTTC AAGTGCCGTG AACTGATTG TACATATTTA 300
 20 TAAAAATCTA TTCAGAAATT GGTCCAATAA TGCACGTGCT TTGCCCTGGG TACAGCCAGA 360
 GCCCTTCAAC CCCACCTTGG ACTTGAGGAC CTACCTGATG GGACGTTTCC ACGTGTCTCT 420
 AGAGAAGGAT TCCTGGATCT AGCTGGTCAC GACGATGTTT TCACCAAGGT CACAGGAGCA 480
 25 TTGCGTCGCT GATGGGGTTG AAGTTTGTTT TGGTCTTGT TTCAGCCCAA TATGTAGAGA 540
 ACATTTGAAA CAGTCTGCAC CTTTGATACG GTATTGCATT TCCAAAGCCA CCAATCCATT 600
 30 TTGTGGATTT TATGTGTCTG TGGCTTAATA ATCATAGTAA CAACAATAAT ACCTTTTTCT 660
 CCATTTTGTCT TGCAGGAAAC ATACCTTAAG TTTTTTTTGT TTGTTTTTTG TTTTTTTTGT 720
 35 TTTTGTTTTC CTTTATGAAG AAAAAATAAA ATAGTCACAT TTTTAATACY AAAAAATGGA 780
 CAAAAAAGT CGAGGGGGG 799

40

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

50 AAAGACTCTA ACATCCATGA GCTTGAACAT GAGCAAGAGC CTACTTGTGC CKSCCAGATG 60
 GCTGAGCCCT TCCGTACCTT CCGAGATGGA TGGGTCTCCT ACTACAACCA GCCTGTGTTT 120
 55 CTGGCTGGCA TGGGTCTTGC TTTCCTTTAT ATGACTGTCC TGGGCTTTGA CTGCATCACC 180
 ACAGGTACG CCTACACTCA GGGACTGAGT GGTTCATCC TCAGTATTTT GATGGGAGCA 240
 60 TCAGCTATAA CTGGAATAAT GGGAACTGTA GCTTTTACTT GGCTACGTCG AAAATGTGGT 300

	TTGGTTGGGA CAGGTCTGAT CTCAGGATTG GCACAGCTTT CCTGTTTGAT CTTGTGTGTG	360
	ATCTCTGTAT TCATGCCTGG AAGCCCCCTG GACTTGTCCG TTTCTCCTTT TGAAGATATC	420
5	CGATCAAGGT TCATTCAAGG AGAGTCAATT ACACCTACCA AGATACCTGA AATTACAAC	480
	GAAATATACA TGTCTAATGG GTCTAATCT GCTAATATTG TCCCGGAGAC AAGTCTGAA	540
10	TCTGTGCCA TAATCTCTGT CAGTCTGCTG TTTGCAGGCG TCATTGCTGC TAGAATCGGT	600
	CTTTGGTCCT TTGATTTAAC TGTGACACAG TTGCTGCAAG AAAATGTAAT TGAATCTGAA	660
	AGAGGCATTA TAAATGGTGT ACAGAACTCC ATGAACTATC TTCTTGATCT TCTGCATTTC	720
15	ATCATGGTCA TCCTGGCTCC AAATCCTGAA GCTTTTGGCT TGCTCGTATT GATTTCAGTC	780
	TCCTTTGTGG CAATGGGCCA CATTATGTAT TTCCGATTTC CCCAAAATAC TCTGGGAAAC	840
20	AAGCTCTTTG CTGCGGTCC TGATGCAAAA GAAGTTAGGA AGGAAAATCA AGCAAATACA	900
	TCTGTTGTTT GAGACAGTTT AACTGTTGCT ATCCTGTTAC TAGATTATAT AGAGCACATG	960
	TGCTTATTTT GACTGCAGA ATTCCAATAA ATGGCTGGGT GTTTTGCTCT GTTTTACCA	1020
25	CAGCTGTGCC TTGAGAACTA AAAGCTGTTT AGGAAACCTA AGTCAGCAGA AATTAACTGA	1080
	TTAATTTCCC TTATGTTGAG GCATGGAAAA AAAATTGGAA AAGAAAACT CAGTTTAAAT	1140
30	ACGGAGACTA TAATGATAAC ACTGAATTCC CCTATTTCTC ATGAGTAGAT ACAATCTTAC	1200
	GTAAAAGAGT GGTTAGTCAC GTGAATTCAG TTATCATTTG ACAGATTCTT ATCTGTACTA	1260
	GAATTCAGAT ATGTCAGTTT TCTGCAAAAC TCACCTTGT TCAAGACTAG CTAATTTATT	1320
35	TTTTTGCATC TTAGTTATTT TTA AAAACAA ATTCITCAAG TATGAAGACT AAATTTTGAT	1380
	AACTAATATT ATCCTTATTG ATCCTATTGA TCTTAAGGTA TTTACATGTA TGTGGAAAAA	1440
40	CAAAACACTT AACTAGAATT CTCTAATAAG GTTTATGGTT TAGCTTAAAG AGCACCTTTG	1500
	TATTTTATT ATCAGATGGG GCAACATATT GTATGAAGCA TATGTAGCAC TTCACAGCAT	1560
	GGTTATCATG TAAGCTGCAG GTAGAAGCAA AGCTGTAAAG TAGATTTATC ACACAATGAC	1620
45	TGCATACAGA CTTCAAATAT GTCAATAGTT TGGTCATAGA ACCTAGAAGC CAAAAGCCAC	1680
	ACAGAAGGCG AAGAATCCCA ATTAACTCA TGTATCATC ATTAGTGATC TGTGTTGTAG	1740
50	AACATGAGGG TGTAAGCCTT CAGCCTGGCA AGTTACATGT AGAAAGCCCA CACTTGTGAA	1800
	GGTTTGTGTT TACAAATCAC TTGATTTAAC ACACTCAGGT AGAATATTTT TATTTTACT	1860
	GTTTTATACC CAGAAGTTAT TTCTACATTG TTCTACAGCA AGAATATTCA TAAAAGTATC	1920
55	CCTTTCAAAT GCCTTTGAGA AGAATAGAAG AAAAAAGTT TGTATATATT TTA AAAAATT	1980
	GTTTTAAAG TCAGTTTGCA ACATGTCTGT ACCAAGATGG TACTTTGCCT TAACCGTTTA	2040
60	TATGCACTTT CATGGAGACT GCAATACGTT GCTATGAGCA CTTCTTTTAT CCTTGGAGTT	2100

TAATCCTTTG CTTTCATCTTT CTACAGTATG ACATAATGAT TTGCTATGTT GTAAAATCTT 2160
TGTAATAAAT TTCTATATAA AATATTTGAA ACTTAA 2196

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(2) INFORMATION FOR SEQ ID NO: 283:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCAGTTAAGG CTTCTGATAA GGAAAGAGAG TCTGAACAGA GCACACACAT CTGGAGCTCC 60
20 AGGAGTGGGG GATGCAGCAT CAGATTCAT CTTGAATTTC TGCTAAAATA CTTTGACTC 120
ATAATGGATC TCAACAAAGA TCTGTATTTT ATCTGTGGCT CCATCTTCCC TCTGGGTCAA 180
GTAGATGTTA AGCTGGACCT TGGCAGCCT CTTAACATGA AGAGATCTAG CTAGACAGAC 240
25 AGACTCCCC ATTTATGGGA ACAAGAATTC AATTTATCT CTATTTATAA AACATTTTTT 300
TAAAGTGCTT TGGGTATAAA AATCTAAATG TCTGCGGTGT GATCAGTCAG GAGCACGTAA 360
30 CTATCACTCT TCGCATCCTT TGGTCACTGG GAGATCCTTT GGGGGCTGGG AGGTCCTTCT 420
GTCCCAGGCT AAAGGAAAAG CTTTACAAGG GTAAGAGCCA CAGAACCCTC GGCAAGAAAG 480
GCCGGTCAGG GAGAATGAAT GGTACAGAGA GGAAAGGAAG GAAAGGGGGT GGAACAGAGG 540
35 TAGAAGGCAA GGAAGGGATG COGCACTGGA GACCGATGGG GAACTCTTAA TTGTGCAAGA 600
GGGAGGATCT TCCTTCTTGA ATGCTGAACA CAGCTAGTCT GAACCTTCCT TGGAAAGTCC 660
40 AGCTGTTTGC CCATGCATAG GGCCAACTCT CCCTGCAAAG CAGCAAATGT GGCTTCTATC 720
AGGAAGGAAA AGTATCCATC AGTGTGACAA GAGGTCACCT TCGAACTTGC ATGAACTCCT 780
TGCGCAGCCA CAAAGAGTCC TGGTAGAAGT GAGGATCGCC TAGTCTTACG GCTGTCCGTT 840
45 TATAGAAGTA GCAGTACAAC ACTGCTGCTA GTCTCTGGAA TACAAACAGC ATTTGAAGTC 900
CATCTGTCCA TATGAAGCTG TTGGAGTTTT TCCAGCGTAA GTTCATGACC CAGACATGAA 960
50 GGGAGATGCT GAGGGCAAAG TACACAGCTG TCAGGATGAT GGTCCCTTTG AACTTATGGA 1020
ATAGGAGGTT GACCAGGCCA GCCTGGAAGA CGAAGGTGTT GAAGAACATG AGGAAATGA 1080
TGATGATGTT GAAGAGGACT GCAATATCCT GGATGCACTG AGGGAGAGGY TTCTAGTTCC 1140
55 TTTGAATGAG AGCTGTTTCC CTGCTCTAA GGCAAGCACC TCCAA 1185

60

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1634 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

10 AGGGAAAGGG GAGGGTAGCG GGAGGGTAGC AGGTGAGTTC CTAGGGCTGG AAGGTTTAGC 60
 AGCAGCCTGG TGCAGTGCCC TGTCAATCAAG ACAAACCCAC GGTCCCTMCTG GGTGCCTACC 120
 15 AAGCTTGGTT TGTACAAAAG CAAGGTGGGA GTCTATTTTT GTACATGAGA TACATCACAC 180
 TTACCTGTGG GCCAGTATIG TGAAGTGAGT CTGAGTTGTT TACACTGATG CCTTCCCTGC 240
 20 CCACCACAAA TTGTGTACAT AGTCTTCAGA TGATACCACC CCTTTCCCCA GCTCCCAACC 300
 AAGAGCTGGT TCTAGGCCTG TGTATATGT CATATTTAGC STTTTATAT ATGACCTTTG 360
 ATTTCTGTG TTTGTATTT AGCACAGTGT ATGCACCTTC ATTTAAATAC ATCTGTGTGC 420
 25 ATACAGATAC GCATATATGT GTGTGCGTAT GCATATATCT CTCATCTGTA GTTTCCAAGA 480
 GTTCAGCTGA AGCAGATGGA GTCCTGCAGC CCAGGAGACA CCCTGCATCC CTGCTAATAG 540
 TGTITGCCAC AAGTATTAGT GAGTCTTCCT TATTAATATT TTCATTTTCAG AAGACTGAAG 600
 30 CAAAGCTGAT AGTGTITGCT GTTCTTTTGG CAGCTAAGTG AGGGTCTTGG GATGACTTGC 660
 TGTGTTCCTC AAGCTGCACT TTGGGGCCAT CTCTGCAGTA TTAGCCCCCT TTTTGCTTGG 720
 35 TGGTACTCTG TCTGTGCCG TGTGTGTGTG TGATAGTCAC TCTTGCATGG CTTCCATGTC 780
 TGGTTTGTGG CATTTGGGGA TAAGGTGCTG AAGCCAGAGC ATTTGCAGTT TGTITGAGGC 840
 CTCGTGCCA ATGATAGATC ACTCCTGTG ACCTGGTATG TCTGCTTGCT TGCTGCTTTT 900
 40 CCTTGCTTTC TCTTGGAAGA GGAAAGGACT CTGGTCAGGC CCAGGCTGAG TGAGATGAGC 960
 TGCAGCTGGC TCATGGCCTT CTTAGAGCAG AGAGAGGAGT ATGTCATTTT ACTAAGTTCC 1020
 45 TAAACAAACA TTTATGCAGG CAACACTCCT TGCAGATCCA GAAACTGAGG CACAATAGGG 1080
 TTATGACTTG CTCAAGAATA TGTAGCTGCT AGGGGTAAA TCAAGGCATC ACAATTCTG 1140
 50 TTCAGCGGC AGGAATAGGC TGTGAATTGC TAGCACTTTT TTTTTTTAAG CAATTACTTT 1200
 TTGACTTGTT CCTCTGAAAG TGCAAGAGGC GTACACCTTT CCCAAATGTA GACTAGAATC 1260
 TGCAGGATGC CACCCACTGT ATAGTTCTGC TTTCCCAGAG AGGAAGAACT TTTAGAAACC 1320
 55 AAATGATCTT AATTGTTATT GCCACCCCT GGCTTTTCCG GGTAGAAAAT TCACAGTAGG 1380
 AATGATGTT AAGAGAGAGT GCTTGGAACC ATGGGTTAAC AGGAAAGGCT ACCTAACTTC 1440
 60 ACATATCTGC AACCAGAGCA GCCACCAAGC ATTACTTAGC AGCAGGAAAA TGATTGTATT 1500

TGAGTTCTCG TGTGTCCAAA ACTGAGGCAC CATGTTCTTT GAAACATGC CACCTCAAGG 1560
 CTGGGCGCGG TGGCTCACAC CTGTAATCCC AGCAVTTTGG GGAGGCCSAG GCGGGGCGG 1620
 5 KTTCAACGGG GGTC 1634

10 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

20 TTCCCCCAG GTTGGCTTCC TCGATTCTT TTTCTTGGTA TCAACGTTT ATTGAAGAA 60
 CAACCCCTC TTTGTCAACC TCAATAATGA GCTCACTGTG GAGGAGCAGC TCGGGCACAG 120
 CTCMCCGYA TGGTCATTGT TACCCCCAA GACCGCAAAA ACTCTGTGTG GACACAGGAT 180
 25 GGACCCTCAG CCCAGATCCT GCAGCAGCTT GTGGTCCTGG CAGCTGAAGC CCTGCCCATG 240
 TTAGAGAAGC AGCTCATGGA TCCCCGGGA CCTGGGGACA TCAGGACAGT GTTCGGGCGG 300
 30 CCCTTGGACA TTTACGACGT GCTGATTGGC CTGTYTCTC GCCATATCCC GCGGCACCGC 360
 AGGCTTGTGG ACTCGCCAGY TGCTCTCTC TGCCGGGGCC TGCTCAGCCA GCGGGGGCCC 420
 TCATCCCTGA TGCCCGTGCT GGTATATGAT CCTNCTCAGC TCTATCTGAC GCAGCTCAGG 480
 35 GAGGCCTTTG GGGATCTGGC CCTTTCTTC TATGACCAGC ATGGTGGAGA GGTGATGGT 540
 GTCTCTGGA AGCCACACG CTTCAGCCG CAGCCCTTCA AGGCCTCCAG CACAAAGGGG 600
 40 CGCATGGTGA TGTCTCGAGG TGGGGAGCTA GTAATGGTGC CCAATGTTGA AGCAATCCTG 660
 GAGGACTTTG CTGTGCTGGG TGAAGGCTG GTGCAGACTG TGGAGGCCG AAGTGAGAGG 720
 TGGACTGTGT GATCCAGCT CTGGAGCAAG CTGTAGACGG ACAGCAGGAC ATTGGACCTC 780
 45 TAGAGCAAGA TGTCAGTAGG ATGACCTCCA CCTCCTTGG ACATGAATCC TCCATGGAGG 840
 GCCTGCTGGC TGAACATGCT GAATCATCTC CAACAAAACC CAGCCCCAAC TTTCTCTCTG 900
 50 ATGCTCCAGC ATTGGGGCAG GGCATGGTG GCCCATGTAG TCTCTGGGC CTCACCATCC 960
 CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA GGAAGTGAAC CCAGGAGATC CATCCACCTA 1020
 TTAGCCCTGG GCCTGGACCT CCTGCGATT TCCACTCCT TTCTTAGTCT TCTTCCAGAA 1080
 55 ACAGAGAAGG GGATGTGTGC CTGGGAGAGG CTCTGTCTCC TTCCTGCTGC CAGGACCTGT 1140
 GCCTAGACTT AGCATGCCCT TCACTGCAGT GTCAGGCCCT TAGATGGGAC CCAGCGAAAA 1200
 60 TGTGGCCCTT CTGAGTCACA TCACCGACAC TGAGCAGTGG AAAGGGGCTA TATGTGTATG 1260

AATAGACCAC ATTGAAGGAG CACAATGCCC TCCTGTGTGTG ATGCCACTTC CCAGGGTGGA 1320
 GACAGTGGAA AAGAACCGAG GACAGGAAAG GATTGGGTAG GTGAAGGGGT CAGGGGACTG 1380
 5 GTAGTCACCC AATCTTGGAG AGGTGCAAAA AGCACTGGGG GCTACCCGTT AGCTGCATCT 1440
 GCCCTGGCTG TTTGCCCGTT CATGTCACAA ACTGCCACTA CTATGTACCT GCAGTGGGGT 1500
 10 TGCAGAGATG GGGGAGACTC AAGTCTTACT CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG 1560
 AATGCTGCCT CCTTTCAGTC TGGTCTACAC CCACCTTCTG GTAGCCTCTC TGCTTCCTGT 1620
 AATTCTGGCT GTTTTTCAG ACTCAGCTCA AATAGTGCCC CTCCTTAAGC CCATCCCTCG 1680
 15 CCCCCAGCCT GAGGTGATCT TTCCCTCCTC TGAAGTATTA GAGCAGTTAC TGTCTGTTC 1740
 GTTCGTTTGG CAGGCACACA CAGTGGCATA AATCTATTG TTTTGAAGTC TGATT 1795

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(2) INFORMATION FOR SEQ ID NO: 286:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCTGCTTTTCG GTGCTGCGTG TACTGCTGGG CGGCTTCTTC GCGCTCGTGG GGTGGCCAA 60
 35 GCTCTCGGAG GAGATCTCGG CTCCAGTTTC GGAGCGGATG AATGCCCTGT TCGTGCAGTT 120
 TGCTGAGGTG TTCCCGCTGA AGGTATTTGG CTACCAGCCA GATCCCTGA ACTACCAAAT 180
 AGCTGTGGGC TTTCTGGAAC TGCTGGCTGG GTTGTGCTG GTCATGGGCC CACCGATGCT 240
 40 GCAAGAGATC AGTAACTTGT TCTTGATTCT GCTCATGATG GGGCTATCT TCACCTTGGC 300
 AGCTCTGAAA GAGTCACTAA GCACCTGTAT CCCAGCCATT GTCTGCCTGG GGTTCCTGCT 360
 45 GCTGCTGAAT GTCGGCCAGC TCTTAGCCCA GACTAAGAAG GTGGTCAGAC CCACTAGGAA 420
 GAAGACTCTA AGTACATCA AGGAATCCTG GAAGTAGAGC ATCTCTGTCT CTTATGCCA 480
 TGCAGCTGTC ACAGCAGGAA CATGGTAGAA CACAGAGTCT ATCATCTTGT TACCAATATA 540
 50 ATATCCAGGG TCAGCCAGTG TTGAAAGAGA CATTTTGTCT ACCTGGCACT GCTTCTCTT 600
 TTTAGCTTTA CTACTCTTTT GTGAGGAGTA CATGTTATGC ATATTAACAT TCCTCATGTC 660
 55 ATATGAAAAT ACAAATAAG CAGAAAAGAA ATTTAAATCA ACCAAAATTC TGATGCCCCA 720
 AATAACCACT TTTAATGCCT TGGTGTAAAT ATACCTCTGA ACTTTTCTCT GTGCCCTTAA 780
 ACAGATATAT ATTTTCTTTT AATGAAAATA AAACCATATA TCCTATTTTA TTTCTCTCTT 840
 60

TTAAAACCTT ATAACTA

858

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(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60
GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120
20 GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
TACCAGCCAG ATCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAACT GCTGGCTGGG 240
TTGCTGCTGG TCATGGGCC ACCGATGCTG CAAGAGATCA GTAACITGTT CTTGATTCTG 300
25 CTCATGATGG GGGCTATCTT CACCTTGSCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
CCAGCCATTG TCTGCCTGGG GTTCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCAG 420
30 ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600
35 ATTTTGCTA CCTGGCACTG CTTTCTTTT TTAGCTTTAC TACTCTTTG TGAGGAGTAC 660
ATGTTATGCA TATTAACATT CTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
40 TTTAAATCAA CCAAATTCT GATGCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780
TACCTCTGAA CTTTTTCTG TGCCTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
AACCATATAT CCTATTTTAT TTCCTCCTT TAAAACCTTA TAACTATAA MAAAAAATAA 900
45 AAAAAAATAA CTCGA 915

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(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1517 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

	CCTGTGGCA ACTAGTGGGT CCCCCGGCT GCAGNAATTC GGCAGTGGT TCTGNGTCTG	60
	AAGATACTCT GAGTTCCTCT GAGAGATCCA AAGGCTCCGG GAGCAGACCC CCAACCCCA	120
5	AAAGCAGCCC TCAGAAGACC AGGAAGAGCC CTCAGGTGAC CAGGGGTAGC CCTCAGAAGA	180
	CCAGCTGTAG CCTCAGAAG ACCAGGCAGA GCCCTCAGAC GCTGAAGCGG AGCCGAGTGA	240
	CCACCTCACT TGAAGCTTTG CCCACAGGAC AGTGTCTGACA GACAAGAGTG GGCACAGTG	300
10	GAAGCTGAAG TCCTTCCAGA CCAGGGACAA CCAGGGCATT CTCTATGAAG CTGCACCCAC	360
	CTCCACCTC ACCTGTGACT CAGGACCACA GAAGCAAAG TTCTCACTCA AACTGGATGC	420
15	CAAGGATGGG CGCTTGTTC AATGAGCAGAA CTTCTTCCAG CGGGCCGCCA AGCCTCTGCA	480
	AGTCAACAAG TGGAAGAAGC TGTACTGAC CCCACTGCTG GCCATCCCTA CCTGCATGGG	540
	TTTCGGTGT CACCAGGACA AATACAGGTT CTTGGTGTTA CCCAGCCTGG GGAGGAGCCT	600
20	TCAGTCGGCC CTGGATGTCA GCCCAAAGCA TGTGCTGTGC AGAGAGGTCT GTGCTGCAGG	660
	TGGCCTGCCG GCTGCTGGAT GCCCTGGAGT TCCTCCATGA GAATGAGTAT GTTCATGGAA	720
25	ATGTGACAGC TGAAAATATC TTGTGGATC CAGAGGACCA GAGTCAGGTG ACTTTGGCAG	780
	GCTATGGCTT CGCNTCCGC TATTGCCAA GTGGCAAACA CGTGGCCTAC GTGGAAGGCA	840
	GCAGGAGCCY TCACGAGGGG GACCTTGAGT TTCATTAGCA TGGACCTGCA CAAGGGATGC	900
30	GGGCCCTCCC GCCGCRGYGA CCTCCAGAGC CTGGGYTAMT GCATGCTGAA GTGGYTCTAM	960
	GGGTTTCTGC CATGGACAAA TTGCCTTCCA AMAMTGAGGA CATCATGAAG CAAAAACAGA	1020
35	AGTTCCTTG GGATTCATTT TAATGTAAGC TKGACTTTGT CATGCCAGAA ACAAGGCTCG	1080
	GTCACCGTCA GCAGTTTGA GTTTTCCACC TCCWCCAGT TCCTCCGTGT GGTTGACCCA	1140
	GATATCTCCG TTATGCAGCC GCCTCCGGG GACCACCTCC CTCCCTTTGA GTCAGCCACA	1200
40	GACAGCCTAC TTGACGGCCC CGCTGGCCCC CACATTCAC TGAAGTGTGC GGATGCCACA	1260
	GTGACCCCT CTCAGGCACA GCATGACCTC CTGAAGTGA GCCTGCTTGC TTTGAACCTA	1320
45	CCAGTTAAAA TCTCTCAA ATGTTTGGAT ACCGCCATT GGCCCTCAC AGCCACGAGC	1380
	TCCCTGACCA GTGTGCGTGT GTGTGTGTGT GTGTGTCTGT GTGTGTGCTT GGGACGGGTG	1440
	GGGAGGTCAC CTTTGGGTGT GCGGTGTGCC CCCAGGACCT GTAAGTAATA AAATCTTTAT	1500
50	TTCCAAAAA AAAAAA	1517

55

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3865 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5	TGGAGGGGGG GAGCTTCCTT GAGCAGTGGG CCCAGGCCTG GCCCTCCACA CTTCATTCTC	60
	TGACCTTTCT CTCTCCTCAT TTCGGTGCAT GTCCTTTCTG CAGCTGCCTT TCAGCACAGG	120
10	TGGTTCCACT GGGGGCAGCT AACGCTGAGT GACAAGGATG GGAAGCCACA GGTGCATTTT	180
	ACTCAAGTCT TCTCTAGTCA ATGAGGGGCA CCCAGTGCTT CTAGGGCAGG CTGGGTGGTG	240
15	GTCCCCTAGG TATCAGCCTC TCTTACTGTA CTCTCCGGGA ATGTTAACCT TTCTATTTC	300
	AGCCTGTGCC ACCTGTCTAG GCAAGCTGGC TTCCCCATTG GCCCTGTGG GTCCACAGCA	360
	GGGTGGCTSC CCCCCAGGGC CACCGCTTCT TTCTTGATCC TCTTTCTTCA ACAGTGACTT	420
20	GGGCTTGAGT CTGGCAAGGA ACCTTGCTTT TAGCTTCACC ACCAAGGAGA GAGGTTGACA	480
	TGACCTCCCC GCCCCTCAC CAAGGCTGGG AACAGAGGG ATGTGGTGAG AGCCAGGTTT	540
25	CTCTGGCCCT CTCCAGGGTG TTTTCCAATA GTCACTACTG TCTTCTCCTT GTAGCTAATC	600
	AATCAATATT CTTCCTTGC CTGTGGGCAG TNGGAGAGTG CTGCTGGGTG TACGCTGCAC	660
	CTGCCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTTCCTGCTC AGAGCTCCTG	720
30	ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT GCATGAAACC AGGCCCTGGC	780
	AGCAACCCCTG GGAATGGCTG GAGGTGGGAG AGAACCTGAC TTCTCTTTCC CTCTCCCTCC	840
35	TCCAACATTA CTGGAACCTT ATCCTGTTAG GATCTTCTGA GCTTGTTTCC CTGCTGGGTG	900
	GGACAGAGGA CAAAGGAGAA GGGAGGTCT AGAAGAGGCA GCCCTTCTTT GTCTCTGGG	960
	GTAAATGAGC TTGACCTAGA GTAAATGGAG AGACCAAAG CCTCTGATTT TTAATTTCCA	1020
40	TAAATGTTA GAAGTATATA TATACATATA TATATTTCTT TAAATTTTGG AGTCTTTGAT	1080
	ATGTCTAAAA ATCCATTCCC TCTGCCCTGA AGCCTGAGTG AGACACATGA AGAAAACGT	1140
45	GTTTCATTTA AAGATGTTAA TTAAATGATT GAAACTTGGC TGTGGCTACT GCTTCTTAAT	1200
	GTGGGGGGA CAGGCGAGTG GTCTGGGCC ACATTTAGAA GGGAAAATGT TTTGCCTGCT	1260
	GCACACATTG GACCCAAGTA TGGGCTCTT CTGCCTAGTA CTGCCAAAGG GACTGTTAAG	1320
50	GTGTCTGTG CATCTTCTAC CCCCCACCC CCATTACGGG TAAAGGRAAC CCCAGACTAG	1380
	GTGAGGGGCC AGCAGCTGCC TCACATGTG TTCTCTCCTG AGATGGTCCA GCTCACATCC	1440
55	AGACACCTTG TTCAGACATT TTATTGAAT TTATGACAGT GATGGGGATT TGA CTGAGAT	1500
	GCCTTATGGA GAAGTACCCC ACCCTCTATG AAGACAGAAT CACTCTCTGC CATTCATTCT	1560
	GCCTGATGCT AACACACGC AGCTGATTTA GGGAGTGTCC CAGCCTAGCT GGATCAAGGG	1620
60	AAATTCCAGG AGCCCTGGG CAGGCCCTGG NCCCCAGTGC CAAGCCTCAG AGTAAGCAGA	1680

	CATTGGGAAA GTTGCCAACC ACTTGGTAGA CCACTAGGTT CTCTGTTTTC CCTTCCCTTT	1740
	CCTTTTCAAA TCCCACAGTT TCCTGTTGGG GAGAAGCTGT AATTAGCCTA GTCCAGGTAC	1800
5	CAGATCCCAG CTAGGGGCGC AGCTGNCITG GATAACTCCA AGAAAACCTG GGCACCAGTA	1860
	TTTTTCCAAT TATAAGGACT GTGGCATAAA TTTTAAATG AGTTATATTG AAACCAGATT	1920
10	TCTCCAGCTG CCAAGGAAG AAGGTAGGCG TGGACTCCCT GCTGTGGCCC AGCCCTTGTT	1980
	AGGGGTGGT CTCTCACTGC AGCCAGACAG GATGATCCTG GGTCTGGGG AGGGTAAGCT	2040
	GCCCTTGCC GAGTCTGCA CCGAATAAAG AGTCCAAACC CGCTGCTTCC GTGTCTGAG	2100
15	AGATGGGTAA ATGGGTGATG GATGGAGCAG ACTGAAGAGA CAGCAGATGA CTCAGTGGTG	2160
	GAAGAAGGGG GGAAGATGCT GGGCTGGCTA GCTAATGTTT CCCCCTTTCA GCGATTTACA	2220
20	GGAAATGGAG CCCAGCTTGG TCATGAAGTT GGTTCCTTC CACTGTGCGA TGCACTCCTC	2280
	AGAAATTTTG AAGTCAGCCT GCAACTTCTC GAAGACTTTC TTCTTGGGCT TGAGCTCCTC	2340
	ATCTGGTTGG CCCTTTTCAT AGCCCTTCAC AAACACGTGC TCACCAGGAG CAGAGCCTGC	2400
25	CGGAGGGTCC AGAGGTTCOA CTGGCGGTTT ATCCCTTCTA TAGAAGCACA CAGAAGCATG	2460
	CCTTGGGACT CGACTCCTCT CATCTTCTGG GGTTCAGGT TGCACAGCAC CACTACCAGC	2520
30	CTGTCTGCA GTTCTCTCTT GGGCAGAAC TGTACCAGGC CGCTCACCAC AGTCCGTGGT	2580
	TCAGCTTCCC CCACGTCAAT CTTCTCTACA TACAGGCTGT CTGCATCTGG GTGCTTCTCC	2640
	ACAGTGATGA TTTTCCCCAC ACGGATATCC AGCCGGGATG GGATGACCTC CTCTGGTTCT	2700
35	GAATCTTGG CAGGCCTTTG GCCATTGGCT TCTGCTTTGA GGGATCTGGG TAGGCAGCGC	2760
	TGGCCAGTTT TTTTCAAGGCA GGGGTATTAA ACTTTTCCCG GATGGATCC AGCAACTTGT	2820
40	TCAGTGGGAC TTCAACAGAA TTCTTCAGGT CTCCAGGATG TACAACCTCA GCAGCAAAGT	2880
	CCTTTTCCAG GTCCACGTAA GCTGTGTAGG TTTTGTTC ACCCCATTTC TCATCTGTGA	2940
	GGATCACAAA CTCGGACTTA AGGGGAAAAA GGACATGCTT GATGAAGGAC AGAACCCCAT	3000
45	TGTTCTCCAC ATTTCTTGGC TCACAGAAGG CCTTCTTCAG TTTTTCCTTC ACATCCTCCT	3060
	TCCGATCAAG GAGATCAATC TTGGACTCCT CTCTGAAGA GCTCATTTTG CTGCCTGTGA	3120
50	ATCCTGGAAC CATAGGATTC ATCAGATGGA CCCGTTTGA ATAGCCAAGT GCAGGGAGGT	3180
	ACTTCTCTGC AAAGGTGAAA ATCTTCTCTT GATCAATGCC TCCAAATTGG GCATCTACTT	3240
	TTAAATACTC TTCATCCAAA GCCTGCAGTC CGGGGTATAA GAGGCCACTC AGCAAAGGGT	3300
55	GCTCCACCTG CTTTACCACC TCAGTCCAG CCTTCTTGA ATCGTGCTGT GTGACCACGG	3360
	AGGAGAGTCT GTACACATCT AGTGTGTA CTCTGCTGAG CTGGTAATCA GTGCCTTTGA	3420
60	TGAACCTGAG CTTCTCCAAG GGCACACCAA TGCTCTCCAG CATTGCTTTG ATCACAATCT	3480

CATAGTAACT GACTCGGAGT TCTAGAAGTT CCCATGGGGC TTTCATGTTA TCCAGGTATG 3540
 5 CGTGGAGGTC CGCAAACAGA ATTGTTACCT CACACCCCTGC CTTTAAGAAG TCTGCAATCT 3600
 TTGACATGGG CACAAAGTAA GCCACATGTG GTTTGCCCGT GGTGCGCGTT CCCAGTAAA 3660
 TTTTAAGTTC CCGCTCCTTC AGTATCTCCT TCAGCTTCTC TTCCCCCAGA ACCTCCTGCA 3720
 10 GGTTCGGGGT GATAAGGTGC AGTTTCTCTT CAGGGCTGGG AGCGTCCCCC ATGGTCCGCT 3780
 ACCCCTGCTT CCCCCGCTCA GCGCGGCACC AGAGCCCCCTT CCTGGGTACAC CGTCCCGGCC 3840
 15 GCGTCCGGG AACTGTCACG CGAGT 3865

(2) INFORMATION FOR SEQ ID NO: 290:
 20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1910 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

30 AGGGAGAGGA GGAGAGGGGG TCTGCGCGCG GCCGCTACCC AGAAGCCAGC GGACGGCAGC 60
 ACGGAGTGGG CTGTCCCCGA GCCCAGCCCC GAGCGAGCCC CCCCCCGCC CCGMAGGAC 120
 GCGCCTYCCA GCCAGCCCCA CTCCTAGGAG GAGGGGAGGC GGGAAAGCAG CTCAAGCCTC 180
 35 ACCCACGCC CTGCCCCCAG CCCCCCACT CCCAGGCTCC TCGGACTCG GCGGTCTCTC 240
 CTGGGAGTCT CGGAGGGGAC CGNCTGTGCA GACGCCATGG AGTTGGTGCT GGTCTTCCTC 300
 TGCAGCCTGC TGGCCCCCAT GTCTCTGGCC AGTGCAGCTG AAAAGGAGAA GGAAATGGAC 360
 40 CCTTTTCATT ATGATTACCA GACCTGAGG ATTGGGGGAC TGGTGTTCGC TGTGGTCTC 420
 TTCTGGGTG GGATCCTCCT TATCCTAAGT CGCAGGTGCA AGTGCAGTTT CAATCAGAAG 480
 45 CCCCCGGGCC CAGGAGATGA GGAAGCCAG GTGGAGAACC TCATCACCGC CAATGCAACA 540
 GAGCCCCAGA AAGCAGAGAA CTGAAGTGCA GCCATCAGGT GGAAGCCTCT GGAACCTGAG 600
 GCGGCTGCTT GAACCTTTGG ATGCAAATGT CGATGCTTAA GAAAACCGGC CACTTCAGCA 660
 50 ACAGCCCTTT CCCCAGGAGA AGCCAAGAAC TTGTGTGTCC CCCACCCTAT CCCCTCTAAC 720
 ACCATTCTC CACCTGATGA TGCAACTAAC ACTTGCCTCC CCACTGCAGC CTGCGGTCTT 780
 55 GCCCACCTCC CGTGATGTGT GTGTGTGTGT GTGTGTGTGT GACTGTGTGT GTTTGCTAAC 840
 TGTGGTCTTT GTGGCTACTT GTTGTGGAT GGTATGTGT TTGTTAGTGA ACTGTGGACT 900
 60 CGCTTTCCCA GGCAGGGGCT GAGCCACATG GCCATCTGCT CCTCCCTGCC CCGTGGGCC 960

	TCCATCACCT TCTGCTCCTA GGAGGCTGCT TGTGCCCCGA GACCAGCCCC CTCCCCTGAT	1020
	TTAGGGATGC GTAGGGTAAG AGCACGGGCA GTGGTCTTCA GTCGTCTTGG GACCTGGGAA	1080
5	GGTTTGACGC ACTTTGTCAT CATCTTTCAT GGACTCCTTT CACTCCTTTA ACAAAAACCT	1140
	TGCTTCCTTA TCCCACCTGA TCCAGTCTG AAGGTCTCTT AGCAACTGGA GATACAAAGC	1200
10	AAGGAGCTGG TGAGCCACGC GTTGACGTCA GGCAGGCTAT GCCTTCCGT GGTAAATTTT	1260
	TTCCCAGGGG CTTCACAGAG GAGTCCCAT CTGCCCCGCC CCTTCACAGA GCGCCCGGGG	1320
	ATTCCAGGCC CAGGGCTTCT ACTCTGCCCC TGGGGAATGT GTCCCCTGCA TATCTTCTCA	1380
15	GCAATAACTC CATGGGCTCT GGGACCCCTAC CCCTTCCAAC CTCCCCTGCT TCTGAGACTT	1440
	CAATCTACAG CCCAGTTCAT CCAGATGCAG ACTACAGTCC CTGCAATTGG GTCTCTGGCA	1500
20	GGCAATAGTT GAAGGACTCC TGTTCCTTGG GGGCCAGCAC ACCGGGATGG ATGGAGGGAG	1560
	AGCAGAGGCC TTGCTTCTC TGCTACGTC CCCTTAGATG GGCAGCAGAG GCAACTCCCG	1620
	CATCCTTTGC TCTGCCGTGC GGTGGTCAGA GCGGTGAGCG AGGTGGGTTG GAGACTCAGC	1680
25	AGGCTCCGTG CAGCCCTTGG GAACAGTGAG AGGTTGAAGG TCATAACGAG AGTGGGAACT	1740
	CACCCAGAT CCGCCCCCTC CTGTCTCTG TGTTCCTCGG GAAACCAACC AAACCGTGGC	1800
30	CTGTGACCCA TTGCTGTCT CTGTATCGTG ATCTATCCTC AACAACAACA GAAAAAAGGA	1860
	ATAAAATATC CTTTGTTCM TAAAAAATA AAAAAAATA AGGGGGGGGG	1910

35

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 3276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

45

	GCGACCGTCG TTTGAGTCGT CGCTGCCGCT GCCGCTGCCA CTGCCACTGC CACCTCGCGG	60
	ATCAGGAGCC AGCGTTGTTT GCCCGACGCC TCGCTGCCGG TGGGAGGAAG CGAGAGGGAA	120
50	GCCGCTTTCG GGTTTGTTCG CGCTGCTCGC CCACCGCTG GAAGAGCCGA GCCCCGGCCC	180
	AGTCGGTCGC TTGCCACCGC TCGTAGCCGT TACCCGCGGG CCGCCACAGC CGCCGGCCGG	240
55	GAGAGGCGCG CGCCATGGCT TCTGGAGCCG ATTCAAAAGG TGATGACCTA TCAACAGCCA	300
	TTCTCAAACA GAAGAACCGT CCCAATCGGT TAATTGTTGA TGAAGCCATC AATGAGGACA	360
	ACAGTGTGGT GTCTTGTCC CAGCCCAAGA TGGATGAATT GCAGTTGTTT CGAGGTGACA	420
60	CAGTGTGCT GAAAGGAAAG AAGAGACGAG AAGCTGTTTG CATCGTCCTT TCTGATGATA	480

	CTTGTTCGTA TGAGAAGATT CGGATGAATA GAGTTGTTTCG GAATAACCTT CGTGTACGCC	540
5	TAGGGGATGT CATCAGCATC CAGCCATGCC CTGATGTGAA GTACGGCAAA CGTATCCATG	600
	TGCTGCCCAT TGATGACACA GTGGAAGGCA TTAGTGGTAA TCTCTTCGAG GTATACCTTA	660
	AGCCGTACTT CCTGGAAGCG TATCGACCCA TCCGGAAAGG AGACATTTTT CTTGTCCGTG	720
10	GTGGGATGCG TGCTGTGGAG TTCAAAGTGG TGGAAACAGA TCCTAGCCCT TATTGCATTG	780
	TTGCTCCAGA CACAGTGATC CACTGCGAAG GGGAGCCTAT CAAACGAGAG GATGAGGAAG	840
15	AGTCCTTGAA TGAAGTAGGG TATGATGACA TTGGTGGCTG CAGGAAGCAG CTAGCTCAGA	900
	TAAAGGAGAT GGTGGAAC TG CCGCTGAGAC ATCTGCCCCT CTTTAAGGCA ATTGGTGTGA	960
	AGCCTCCTAG AGGAATCCTG CTTTACGGAC CTCCTGGAAC AGGAAAGACC CTGATTGCTC	1020
20	GAGCTGTAGC AAATGAGACT GGAGCCTTCT TCTTCTTGAT CAATGGTCCT GAGATCATGA	1080
	GCAAATGGC TGGTGAGTCT GAGAGCAACC TTCGTAAAGC CTTTGAGGAG GCTGAGAAGA	1140
25	ATGCTCCTGC CATCATCTTC ATTGATGAGC TAGATGCCAT CGCTCCCAA AGAGAGAAAA	1200
	CTCATGGCGA GGTGGAGCGG CGCATTGTAT CACAGTTGTT GACCCTCATG GATGGCCTAA	1260
	AGCAGAGGGC ACATGTGATT GTTATGGCAG CAACCAACAG ACCCAACAGC ATTGACCCAG	1320
30	CTCTACGGCG ATTTGGTCGC TTTGACAGG AGGTAGATAT TGGAAATCCT GATGCTACAG	1380
	GACGCTTAGA GATTCTTCAG ATCCATACCA AGAACATGAA GCTGGCAGAT GATGTGGACC	1440
35	TGGAACAGTA GCCAATGAGA CTCACGGGCA TGTGGGTGCT GACTTAGCAG CCCTGTGCTC	1500
	AGAGGCTGCT CTGCAAGCCA TCCCAAGAA GATGGATCTC ATTGACCTAG AGGATGAGAC	1560
	CATGATGCC GAGGTCATGA ACTCTCTAGC AGTTACTATG GATGACTTCC GGTGGGCCTT	1620
40	GAGCCAGAGT AACCCTATCAG CACTGCGGGA AACCGTGGTA GAGGTGCCAC AGGTAACCTG	1680
	GGAAGACATC GGGGGCCTAG AGGATGTCAA ACGTGAGCTA CAGGAGCTGG TCCAGTATCC	1740
45	TGTGGAGCAC CCAGACAAAT TCCTGAAGTT TGGCATGACA CCTTCCAAGG GAGTTCTGTT	1800
	CTATGGACCT CCTGGCTGTG GGAACCTTT GTTGGCCAAA GCCATTGCTA ATGAATGCCA	1860
	GGCCAACCTC ATCTCCATCA AGGGTCCTGA GCTGCTCACC ATGTGGTTTG GGGAGTCTGA	1920
50	GGCCAATGTC AGAGAAATCT TTGACAAGGC CCGCCAAGCT GCCCCTGTG TGCTATTCTT	1980
	TGATGAGCTG GATTGATTG CCAAGGCTCG TGGAGGTAAC ATTGGAGATG GTGGTGGGC	2040
55	TGCTGACCGA GTCATCAACC AGATCCTGAC AGAAATGGAT GGCATGTCCA CAAAAAAAA	2100
	TGTGTTTCATC ATTGGCGCTA CCAACCGGCC TGACATCATT GATCCTGCCA TCCTCAGACC	2160
	TGGCGTCTT GATCAGCTCA TCTACATCCC ACTTCCTGAT GAGAAGTCCC GTGTTGCCAT	2220
60	CCTCAAGGCT AACCTGCGCA AGTCCCCAGT TGCCAAGGAT GTGGACTTGG AGTTCTCTGGC	2280

	TAAATGACT AATGGCTTCT CTGGAGCTGA CCTGACAGAG ATTTGCCAGC GTGCTTGCAA	2340
5	GCTGGCCATC CGTGAATCCA TCGAGAGTGA GATTAGGCGA GAACGAGAGA GGCAGACAAA	2400
	CCCATCAGCC ATGGAGGTAG AAGAGGATGA TCCAGTGCCT GAGATCCGTC GAGATCACTT	2460
	TGAAGAAGCC ATGCGCTTTG CGCGCCGTTT TGTCAGTGAC AATGACATTC GGAAGTATGA	2520
10	GATGTTTGCC CAGACCCCTC AGCAGAGTCG GGGCTTTGGC AGCTTCAGAT TCCCTTCAGG	2580
	GAACCAGGGT GGAGCTGGCC CCAGTCAGGG CAGTGGAGGC GGCACAGGTG GCAGTGTATA	2640
15	CACAGAAGAC AATGATGATG ACCTGTATGG CTAAGTGGTG GTGGCCAGCG TGCACTGAGC	2700
	TGGCCTGCCT GGACCTTGTT CCCTGGGGGT GGGGGCGCTT GCCCAGGAGA GGGACCAGGG	2760
	GTGCGCCAC AGCCTGCTCC ATTCTCCAGT CTGAACAGTT CAGCTACAGT CTGACTCTGG	2820
20	ACAGGGGGTT TCTGTTGCAA AAATACAAAA CAAAAGCGAT AAAATAAAG CGATTTTCAT	2880
	TTGGTAGGCG GAGAGTGAAT TACCAACAGG GAATTGGGCC TTGGGCTATG CCATTTCTGT	2940
25	TGTAGTTTGG GGCAGTGAG GGGACCTGTG TGGGGTGTGA ACCAAGGCAC TACTGCCACC	3000
	TGCCACAGTA AAGCATCTGC ACTTGACTCA ATGCTGCCCG AGCCCTCCCT TCCCCCTATC	3060
	CAACCTGGGT AGGTGGGTAG GGGCCACAGT TGCTGGATGT TTATATAGAG AGTAGGTTGA	3120
30	TTTATTTTAC ATGCTTTTGA GTTAATGTTG GAAACTAAT CACAAGCAGT TTCTAAACCA	3180
	AAAAATGACA TGTGTAAAA GGACAATAAA CGTTGGGTCN AAATGGGWRA AAAAAAAAAA	3240
35	AAAAAAGGGG GGGCCCTCTA AAGNCCANN CTTCGT	3276

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50	TTGCAATGGT TGAATTCCCC TCCTCAGGCC AGCCTAGGAG AAGAAGTTCG TAGTCCCAGA	60
	GGTGAGGCAG GAGGCGGCAG TTTCTGGCGG GTGAGGGCGG AGCTGAAGTG ACAGCGGAGG	120
	CGGAAGCAAC GGTCCGTGGG GCGGAGAAGG GGGCTGGCCC CAGGAGGAGG AGGAAACCCCT	180
55	TCCGAGAAAA CAGCAACAAG CTGAGCTGCT GTGACAGAGG GGAACAAGAT GCGGCGCCG	240
	AAGGGAGCCT CTGGGTGAGG ACCCAACTGG GGCTCCCGCC GCTGCTGCTG CTGACCATGG	300
60	CCTTGGCCGG AGGTTCCGGG ACCGCTTCGG CTGAAGCATT TGACTCGGTC TTGGGTGATA	360

	CGGCGTCTTG CCACCGGGCC TGTCAATTGA CCTACCCCTT GCACACCTAC CCTAAGGAAG	420
	AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTT AATTGTGTCAG TTTGTGGATG	480
5	ATGGAATTGA CTAAATCGA ACTAAATTGG AATGTGAATC TGCATGTACA GAAGCATATT	540
	CCCAATCTGA TGAGCAATAT GCTTGCCATC TTGGTTGCCA GAATCAGCTG CCATTGCGTG	600
10	AACTGAGACA AGAACAACCTT ATGTCCCTGA TGCCAAAAAT GCACCTACTC TTTCCCTCTAA	660
	CTCTGGTGAG GTCATTCTGG AGTGACATGA TGGACTCCGC ACAGAGCTTC ATAACCTCTT	720
	CATGGACTTT TTATCTTCAA GCCGATGACG GAAAAATAGT TATATTCCAG TCTAAGCCAG	780
15	AAATCCAGTA CGCACCACAT TTGGAGCAGG AGCCTACAAA TTTGAGAGAA TCATCTCTAA	840
	GCAAAATGTC CTATCTGCAA ATGAGAAATT CACAAGCGCA CAGGAATTTT CTTGAAGATG	900
20	GAGAAAGTGA TGGCTTTTTA AGATGCCTCT CTCTTAACTC TGGGTGGATT TTAAGTACAA	960
	CTCTGTCTCT CTGGTGATG GTATTGCTTT GGATTGTGTG TGCAACTGTT GCTACAGCTG	1020
	TGGAGCAGTA TGTTCCTCTT GAGAAGCTGA GTATCTATGG TGACTTGGAG TTTATGAATG	1080
25	AACAAAAGCT AAACAGATAT CCAGCTTCTT CTCTTGTTGGT TGTTAGATCT AAAACTGAAG	1140
	ATCATGAAGA AGCAGGGCCT CTACCTACAA AAGTGAATCT TGCTCATCTT GAAATTTAAG	1200
30	CATTTTTCTT TTAAAAGACA AGTGAATAG ACATCTAAAA TTCCACTCCT CATAGAGCTT	1260
	TTAAAATGGT TTCATTGGAT ATAGGCCTTA AGAAATCACT ATAAAATGCA AATAAAGTTA	1320
	CTCAAATCTG TGAAGACTGT ATTTGCTATA ACTTTATTGG TATTGTTTTT GTAGTAATTT	1380
35	AAGAGGTGGA TGTTTGGGAT TGTATTATTA TTTTACTAAT ATCTGTAGCT ATTTTGTTTT	1440
	TTGCTTTGGT TATTGTTTTT TTCCCTTTTC TTAGCTATGA GCTGATCATT GCTCCTTCTC	1500
40	ACCTCCTGCC ATGATACTGT CAGTTACCTT AGTTAACAAG CTGAATATTT AGTAGAAATG	1560
	ATGCTTCTGC TCAGGAATGG CCCACAAATC TGTAAATTGA AATTAGCAG GAAATGACCT	1620
	TTAATGACAC TACATTTTCA GGAAGTAAA TCATTAAAAT TTTATTTGAA TAATTAAAAA	1680
45	AAAAAAAAA AANCT	1695

50 (2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1501 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

60 CACTTTCAGC AGTCCTTTGC TCTCTTTGCT TCTACCTCAA ATAGCCCCAG GAGTGGGCTT 60

	TAGTCTCCAA TATGGAGCAT CTCAAGCTTC TCCTGGGGGA TGGGGATTGG GATGGGCAGA	120
5	ATCTGTTTTG GWTCGCCGG TTATTTCCAG TGGGTGTAAA AGCAGAGCTG GGCCTTTCCC	180
	TCTCTTATCC CTGAGGGTGG GTAAGAAGGA CTGTATCTAC ACCTGTTCCT CCCTACCTTC	240
	TCITTTGTGA GGGAGGCCTC ATTCTAAGTT CCTCAAGAGA GTCCCTGGCT TAAAGCTGTA	300
10	GCAAGGGTGT GCTAGGTGGG GGATTGGAG CAAAACCGTC GAGTAGGCAT GATACTGGTA	360
	TGGAGTGGGC CTGCAAAATC AGACAGAAAT GGCTTGAGAA GCCGCAGGGG AGCATGCCTG	420
15	TCTCTCAGTG ATAGAGTATG GGAGGGACCT CCCTAGCTTG GAAAATGAGA ATTGAAGGGG	480
	TTATGAACAA ATAGGATGCC TAGTTGAGGA TGTCCCAA GTTTGTCCA ATCTTATCAT	540
	TAGTAGATTT TATAAGCCAC AGAGACAAAC CAGAAACGGA ATAATGTTAC TTTGGATGCT	600
20	TTATTTTTTT GTTCTAGGTG TGGCTTTGTA CATGCAGAAG AATGCTATAT GCTGCACATT	660
	TTGCCCTTAA AGTCCTACGA CTTTCCCAT TTTAGTCTAA TGGGAAGATA CAGATGTGCA	720
25	AGTCTGCTTT TTTGTTTTTT GTTATTATTT TTTTTTTTTT GCTCTGTGTT ATGGACATTT	780
	TCAGACATGC ACAGAAGTGG AGAGGATGGT CCTTGGACCC MATGTGTCCA TCACCTAGCT	840
	GCATCACTTA TCAGCTATGG TCAACCTGGT TTCATCTGTA TCTCTCTCTT TTCACCTGTA	900
30	TTGTTTTATTG AAAATCCAAG ACACTATGCC AATGCAACCG TGACTACTTT GGGAGATTGG	960
	TAGTCTCTTT TGATGGTGAT AGTGATGGGG TGCACTATCA TAATCACATC AGGTCTGCTT	1020
35	TTTGCTTTTA ATGTAACTA ATGAAGTCC AGAGATGGGC CTTAGAAATG TGTMTTAAGA	1080
	ATTAACAAGG AGTCTCAAAA AGAAATGAGA GGGATGCTTC CTTTNCCTT GCATCTACAA	1140
	AACMAGAGAG AGACTGTCTT GTTGTA AAC TCTTTCAAAA ATTCTGATAT GGTAAAGTAC	1200
40	TTGAGACCCT TCACCAGAAT GTCAATCTTT TTTTCTGTGT AACATGGAAA CTTGTGTGAC	1260
	CATTAGCATT GTTATCAGCT TGTACTGGTC TCATAACTCT GGTMTTGGAA GAATAATTG	1320
45	GAAATGTTG CTGTGTTCTG TGAAAATAAC CTCGCCAAA TAATTAGTAA CTGGTTGTC	1380
	TACTTGGTAA TTTGACACCC TGTTAATAAC GCAATTATTT CTGTGTCTT AAACAGTATA	1440
	AATAGTTGTA AGTTTGCATG CATGATGGAA AAATAAAAAC CTGTATCTCT GTTAAAAAAA	1500
50	A	1501

55 (2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

5	TGANTGTGGT CCCGGGTGCN GATTGGCAGN GCCTCCGCCG CGGCTCGTGG TTGTCCCGCC	60
	ATGGCACTGT CGCGGGGGCT GCGCCGGGAG CTGGCTGAGG CGGTGGCCCG GGGCCGGGTR	120
10	CTGGTGGTGG GGGCGGGCGG CATCGGCTGC GAGCTCCTCA AGAATCTCGT GCTCACCGGT	180
	TTCTCCACACA TCGACCTGAT TGATCTGGAT ACTATTGATG TAAGCAACCT CAACAGACAG	240
	TTTTTGTTC AAAAGAAACA TGTGGAAGA TCAAAGGCAC AGGTGCCAA GGAAAGTGA	300
15	CTGCAGTTTT ACCCGAAAGC TAATATCGTT GCCTACCATG ACAGCATCAT GAACCCCTGAC	360
	TATAATGTGG AATTTTTCCG ACAGTTTATA CTGGTTATGA ATGCTTTAGA TAACAGAGCT	420
20	GCCCGAAACC ATGTTAATAG AATGTGCCTG GCAGCTGATG TTCCTCTTAT TGAAAGTGGA	480
	ACAGCTGGGT ATCTTGGACA AGTAACTACT ATCAAAAAGG GTGTGACCGA GTGTTATGAG	540
	TGTCATCCTA AGCCGACCCA GAGAACCCTT CTGGCTGTA CAATTCGTAA CACACCTTCA	600
25	GAACCTATAC ATTGCATCGT TTGGGCAAAG TACTTGTICA ACCAGTTGTT TGGGGAAGAA	660
	GATGCTGATC AAGAAGTATC TCCTGACAGA GCTGACCCTG AAGCTGCCTG GGAACCAACG	720
30	GAAGCCGAAG CCAGAGCTAG AGCATCTAAT GAAGATGGTG ACATTAAACG TATTTCTACT	780
	AAGGAATGGG CTAAATCAAC TGGATATGAT CCAGTTNAAA CTTTTTACCA AGCTTTTTAA	840
	AGATGACATC AGGTATCTGT TGACAATGGA CAAACTATGG CGGAAAAGGA AACCTCCAAT	900
35	TCCGTTGGAC TGGGCTGAAG TACAAAGTCA AGGAGAAGAA ACGAATGCAT CAGATCAACA	960
	GAATGAACCC CAGTTAGGCC TGAAAGACCA GCAGGTTCTA GATGTAAAGA GCTATGCACG	1020
40	TCTTTTTTCA AAGAGCATCG AGACTTTAG AGTTCATTTA GCAGAAAAGG GGGATGGAGC	1080
	TGAGCTCATA TGGGATAAGG ATGACCCATC TGCAATGGAT TTTGTACACT CTGCTGCAA	1140
	CCTCAGGATG CATATTTTCA GTATGAATAT GAAGAGTAGA TTTGATATCA AATCAATGGC	1200
45	AGGGAACATT ATTCTGCTA TTGCTACTAC TAATGCAGTA ATTGCTGGGT TGATAGTATT	1260
	GGAAGGATTG AAGATTTTAT CAGGAAAAAT AGACCAGTGC AGAACAA'TTT TTTTGAATAA	1320
50	ACAACCAAAC CCAAGAAAGA AGCTTCTTGT GCCTTGTGCA CTGGATCCTC CCAACCCCAA	1380
	TTGTTATGTA TGTGCCAGCA AGCCAGAGGT GACTGTGCGG CTGAATGTCC ATAAAGTGAC	1440
	TGTTCTCACC TTACAAGACA AGATAGTGAA AGAAAAATTT GCTATGGTAG CACCAGATGT	1500
55	CCAAATTGAA GATGGGAAAG GAACAATCCT AATATCTTCC GAAGAGGGAG AGACGGAAGC	1560
	TAATAATCAC AAGAAGTTGT CAGAATTGG AATTAGAAAT GGCAGCCGGC TTCAAGCAGA	1620
60	TGACTTCCTC CAGGACTATA CTTTATGAT CAACATCCTT CATAGTGAAG ACCTAGGAAA	1680

	GGACGTTGAA TTTGAAGTTG TTGGTGATGC CCCGAAAAA GTGGGSSCCA AACAAAGCTGA	1740
	AGATGCTGCC AAAAGCATAA CCAATGGGCA GTGATGATGG AGCTCAGCCC TCCACCTCCA	1800
5	CAGCTCAAGA GCAAGATGAC GTTCTCATAG TTGATTCCGA TGAAGAAGAT TCTTCAAATA	1860
	ATCCCGACGT CATGAAGAAG AGAGAAGCCG CAAGAGGAAA TTAGATGAGA AAGAGAATCT	1920
10	CAGTGCAAAG AGGTCACGTA TAGAACAGAA GGAAGAGCTT GATGATGTCA TAGCATTAGA	1980
	TTGAACAGAA ATGCCTCTAA ACAGAACCCCT CTTACTATTT AGTTTATCTG GGCAGAACCA	2040
	GATTGTTATG TCCTTTGTTC CAAAGGGAAA AAATTGACAG CAGTGACTTG AAAATGATTG	2100
15	TGCTCCCTTT GAAAGCATTC ATTTTGCTAG AACTGTTAGA CACATTGCAG TATGCTGTAT	2160
	TGAAAGTAGG AATATAGTTT TAAAAACCCCT TTGAACAAAG TGTGTGCATA ACCAGTCATG	2220
20	AGATAAACA ACACAATGCA TGTTCCTTT TTAATGTAAA TACCCTTAGG TATCATTAAAT	2280
	AGTTTCAAAA TATTGTGGTT TAGTAAAGTT GATACCTGGT TATAAATATT ATGCCTTAT	2340
	TTTTGGCTAG AAGAAGAATT ATTTTTCAGC TAGATCTAAC CATTTTCATA CTCTTAACG	2400
25	ATTGAAACAG ATTCAAAGAA GTATCGAGTG CTATGCATTG AAACCTGTTT TTAAATGTTA	2460
	GATGGCACTA TGTATATTAA TGTAAACAA TGTAAATTA CTCAAGTTT CAGTTTGTAC	2520
30	CGCCTGGTAT GTCTGTGTAA GAAGCCAATT TTTGTGTATT GTTACAGTTT CAGGTTATTT	2580
	ATATTGATG TTTTGTAAAA CTCAAATAAC GACTATACTT ATGGACCAA TAAATGGCAY	2640
35	TGCATTCTKG TKAAAAAAN NACAGAAAA AAAAAAACA AGA	2683

(2) INFORMATION FOR SEQ ID NO: 295:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

	GGACTCGGG TGGCTCTAAG GGCAGGGAT AGGGCTGGG AGCGCGGCC TGTGGCCCTG	60
50	ACCAGCCCTT TCTCGTGCAG GTTCCACCCC GATGCAGGTG GTCACGTGCT TGACGCGGGA	120
	CAGCTACCTG ACGCACTGCT TCCTCCAGCA CCTCATGGTC GTGCTGTCTT CTCTGGAACG	180
55	CACGCCCTCG CGGAGCCTG TTGACAAGGA CTTCTACTCC GAGTTTGGGA ACAAGACCAC	240
	AGGGAAGATG GAGAACTACG AGCTGATCCA CTCTAGTCGC GTCAAGTTTA CCTACCCAG	300
	TGAGGAGGAG ATTGGGGACC TGACGTTTAC TGTGGCCCA AAGATGGCTG AGCCAGAGAA	360
60	GGCCCCAGCC CTCAGCATCC TGCTGTACGT GCAGGCCTTC CAGGTGGGCA TGCCACCCCC	420

TGGGTGCTGC AGGGGCCCC TGCGCCCAA GACACTCCTG CTCACCAGCT CCGAGATCTT 480
 CCTCCTGGAT GAGGACTGTG TCCACTACCC ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA 540
 5 GAGAGACAGG TACCGGCTGG ACGATGGCCG CCGCGTCCGG GACCTGGACC GAGTGCTCAT 600
 GGGCTACCAG ACCTACCCGC AGCCCTCACC CTCGTYYTTCG ATGACGTGCA AGGTCATGAC 660
 10 CTCATGGGCA GTGTCAACCCT GGACCACTTT GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC 720
 AGCCAGGGCC GTGAAGTCCA GTGCAGGTG TTTGTCCCA GTGCTGAGAG CAGAGAGAAG 780
 CTCATCTCGC TGTGTGCTCG CCAGTGGGAG GCCCTGTGTG GCCTGAGCTG CCTGTGAGC 840
 15 TCACCGGCTA GCCCAGGCCA CAGCCAGCCT GTCGTGTCCA GCCTGAGGCC TACTGGGGCA 900
 GGGCAGCAGG CTTTGTGTGTT CTCTAAAAAT GTTTTATCCT CCCTTTGGTA CCTTAATTG 960
 20 ACTGTCTCG CAGAAATGTG AACATGTGTG TGTGTGTGT TAATTCTTC TCATGTTGGG 1020
 AGTGAGAATG CCGGGCCCT CAGGGCTGTT CGGTGTGCTG TCAGCCTCCC ACAGGTGGTA 1080
 CAGCCGTGCA CACCACTGTC GTGTCTGCTG TTGTGGGACC GTTGTTAACA CGTGACACTG 1140
 25 TGGGTCTGAC TTTYTCTTCT ACAGTCTCTT TCCTGAAGTG TCGAGTCCAG TCCTTTGTG 1200
 CTGTGTCTGT TGCTGTGCT GTTGCTGTG GCATCTTGCT GCTAATCCTG AGGCTGGTAG 1260
 30 CAGAATGCAC ATTGGAAGCT CCCACCCAT ATTGTCTTC AAAGTGGAGG TCTCCCTGA 1320
 TCCAGACAAG TGGGAGAGCC CGTGGGGCA GGGGACCTGG AGCTGCCAGC ACCAAGCGTG 1380
 ATTCTGTCTG CCTGTATTCT CTATTCCAAT AAAGCAGAGT TTGACACCGW MAAAAAAAAA 1440
 35 AAAAAAAAAA AACN 1454

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(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 828 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

50

ACCCTGGCAT GCCCCACAAA CAGATCACCA GCCAGCTTAC ACAGGCATTA ACTCTCTCA 60
 ATGAGGAAGA ATCATTCACT ACTGAGCAAG ACATTTCATAT GATCATTTAA GGAAGTGTTT 120
 55 CCCTTATGTG TTAGCAAGTA TAATCGGCTA ACTCCTAAAT CCCAATGAAT AGTCCTAGGC 180
 TGGACAGCAA TGGGCTGCAA TTAGGCAGAT AAAGACATCA GTCCAGTAA ATGAATCCAT 240
 AGACTCATCT AGCACCAACT ACCATTAGCA CTATGTTAGG AGCTGCAAGG CCCCCAAGTA 300
 60

GAAGATGTGC ATAATGTCTG CTCTTGTTGA GCTCAGGAGA CAATTCAGC ACAGACACTA 360
 CAGTTAACGC TGAAGTCAG CTGCAAGTAA TAGCAWGAAC AGTCAGAAAA ATACCTTATG 420
 5 AGGGGGCAGG GCTGAAGCTG GGCCTTGAAG GATGGATGAA ATTTGGATAG AGAATGAGGA 480
 AGACAGAGGG NCTCCAAGTG AGAGAAGCAT GAAAAATGAG CARGGGCCTG GATCAGTGGG 540
 GTGTATTTCAG AGCACCTYTC CAGATGCACC ATGCATGCTC ACAGTCCCTT GCCTATGTGT 600
 10 GGCAGAGTGT CCCAGCCAGA TGTGTGCCCC CACCCCATGT CCATTTACAT GTCCTTCAAT 660
 GCCCACCTCA AAAGGYACYT CTTCTGTAAA GCTTTCCTK GGTATCAGGA ATCAAAATTA 720
 15 ATCAGGGATC TTTTCACACT GCTGTTTTTT CCTCTTTGGT CCTTCTATCA CTAAAACTCA 780
 TCTCATTCAG CCTTACAGCA TAACTAATTA TTTGTTTTCC TCACTACA 828

20

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 2416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

TCAATTTCCA TTAAGTCAGA TCAGCCATTG TGATTACCA TTTGTCAGGC TCTCAGGTTT 60
 AACAAAACCT ACTATACCA TCATCCTTCA ACAGCCACAG TCTGAATGA GCCAACATTT 120
 35 TTTTTTCTTT GAGAAAGAAG TGGACTGGGG CACAACTTTT AGTCTGAGGG GAGCTAGTGG 180
 AAATCTAGAC AATAGAAGTC ATCGATAGCA GCTTTTCCTC AAATGTGTGA CTCTCAGGG 240
 40 GCTAAACTGC TCTTAGCTTA GAATTATGCT TTAGTAGAGA TCTAGCAGAT AAGTGGGTTA 300
 ATCACTACCA TCCTGTAACT AGTTATATAG CTTCAGACA TGAGGGAGAC ATCAAAACAGG 360
 GATGGAAGCA ACCCAAGGA TATGCAAGAA GGCATGATG AACCCCTTC CCTCTGGCAG 420
 45 GAGAACAAGG CCAACCAAGG GACAGACTGG AAAGCACTTA GATGTTTAAG GAGGAGAAAG 480
 GGAAGCTTT GACCAGTCCT TGCCTTTTC CAAGTTCAGC CAGTCTCCG CTGCTTGCAA 540
 50 CCTCTAGCGC AGTAACATTT GCAGAATTGC AGATTTTCCC CCAGATACTA GGAGGAAAGG 600
 GACTTTGGGG GGTGGGAAG GGTGCTGGT GTTTTAAAAG CATAAGTTAC CTGTTTGCAC 660
 TGTTTTAAGA TAGGAAAAAA AAATAGTGGG CAAGGTGAAC ATCAGACGTA AATTTGTGTG 720
 55 TTTTATTTTT GTCATGCTCT TGAAATGTT TGACCATTTG TAGTATACAC AGTGAACTT 780
 GATTCTCTGT TGCATAAAAC ACTATATTTT TTTGAAATG TTAGTGCCA AAAGCCTCTT 840
 60 CCTCCCTTT CCTTTCTTA TGTACTTCCT TCATACTGC TTTACTGATC AGCCAGGCAA 900

	TAGCCATCCA AGAGCTAGAG CATGAAACAG GGCCCTTTCC AAGTAGGCTC TGGGTGTCCT	960
5	AAGCCAGCGT GTGCCCTCTG GTTTAGTGAG TGTAATAGAG TCCCTGGCAC CTTTCTTTGC	1020
	AAATGAGGCT AACAGACCAG ACTGCAGCAA GTTATCAGAT TCCTCAATCA GATGCACTAG	1080
	GAGTGAGGAG CCCAGGGATG GAGGGGGTTC CTGAAGTATT GCAGTTGGCT GTAGTAGCTG	1140
10	AGTTCTTTTC CATGTTACCG AAAGTGTAGC CAGTTACAGT TTAAGTACAG AAACGGTAGA	1200
	TCAATTCAGC CATGGTAGTG CTGGTTGGCA GGGATTGGTA ACGGAGAGAA CTGCTCATCA	1260
15	GCCAAACTC AAGCCTTGCC TTTTAGGAGG CCACCAGCAG AGGGACTTGG TCCTCCTTGT	1320
	CTGGTACTTG TGTACATGCC GGTGACCTGA GGACTCCACT CACACTGGCG AGCAAAAAGG	1380
	GAGCAGTGAT TCTCTTTTCT CTCCCCACCC CCTGCCCTTT GTTACCAACA CCAGTTTCCC	1440
20	AGGGGGTACA TGAGTTTCTG AATTTTAA AAATGTTTTT GGTMTGGTTT TTCTGGGGAC	1500
	TGATAAGTGC TTTAAGCAAT GTCCATACCC CGTCAAGACT CCCAGCTTAG TCATTTTCTT	1560
25	GTATTTTCT GTTCACAGTA TTTGTGTGTG TGCTGTMTT GGCAGCTCAT TTGGGCTGTA	1620
	TTATATATTG AGTGATGAAT TGATCCTCTT TTTTCCCTAA GGGATATGAA TTGTTTTTCT	1680
	TGTGTATAT TCTGCTTGTG AATAGCTGGA GCAAACCTGG GGCTGACACG CGTAAGSTAG	1740
30	GGCTGCAAAR CGAGAAGAGA GCGGTGGAG TGTACTTGTG CCTGACAGGC TGACCTACCT	1800
	GAGTCTCTGA GCTTTTCAGT CCAAATCTTT GCAAGGCTCA AAATGCCACA GAACCTCTCC	1860
35	TCTTCTCCCC ACTCCCCATG GCAGGGACCG GACCATCCCT ACATGCAACA TGCTGTTCCT	1920
	CCAGCCCCTC CCATTGCCAT GGCAAAACAG GTACCTTTGG GGCATGGGGG CATTACATGG	1980
	GATGCTTGTG TAATCGACCA CCTAGCCTTC TCTCTCCCT CCCGTCTCTC CCCAGAATCA	2040
40	CTTCTTAGGA CACCCGAGCT GCTTGCCAG GGTCTGTGTT CCCTGCTAAC TCCAGAGAAG	2100
	CATCCAGGG CTTTGTGACA GTCTCTAATT CCCTTCCCTT CTCGTAAAGA ATCATATTGT	2160
45	ATAGTAGCTT TCAGACCATA CAGTATTCAT TGGGTACTC CTATTATTAT CAAGTAGCTG	2220
	GAATTGTGAA GGTCCGAGTA GTTAGATCTT TAGCTTTTAT TCCTTATTTT TTGTATTAC	2280
	TCTCCATGTG TATAAATTAT TGATCATGTT GCTGGCTTTT ATAACTCTA AGCGAAGGAG	2340
50	GAGCACTGCC TCAGCCTTTG CACATGGTAA TGAAGCACTG TTTTAAATA AAAGRGRGAA	2400
	MCMCCAAAAA AAAAAA	2416

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(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

	GAATTCGGCA CGAGCCATGC YTGGCCTCTC CTTGATTCTT ACAGTCACTT TGTGGCTGT	60
	TTCTGACTCA GCAGCTACCT GCATTGTGGC CAAAGGATGA CCTATTCTT CTCAGGAGGG	120
10	CAAAAATGTG GAATAGTGTG TGTCCATGCC TCTCCTCATG GGCTACCACC TCTGCCACCG	180
	TGGTTAATCA GTAACAACCA GGAGAGAAGC TGCTGGAAC TACCTCTGGG AACTCCCTGG	240
15	ATGGTTTGGT GCAGGAATGT AGTAGGCATA CACGTGGTTG CGTGGATCTG GGCCCTCCTG	300
	ATGTGAGTAG AGAGGTAAAA GGSCACCATC TCCTTGACCT YTGGGGAAC CATCCACAAA	360
	GAAGATGTTT CCAAGATGCT TCTGAAGATT GSCTAAAAAT AGCCGGTTTC CACCCCGTG	420
20	AATGCATCCA TTCTAGAATG CTCCTTCACC AGGACCAGAG AACTGATTTA CAGAAGTGAC	480
	ATGAAAACAT TCCATCCAG AATTGCAAT ACCTCAAATT NAATTCTAC CTATTAATAA	540
25	NAAAA	545

30 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1530 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

40	GGCTCTGCTG GGCATCATAC TTGTCACTGG GTAAACAGTT TGCCCACTTA CCGCAGATGA	60
	AGCTGCTTGC CAGGGCTCTC CGGCTCTGTG AGTTTGGGAG GCAGGCATCT TCCAGGAGGC	120
	TGGTGGCTGG CCAGGGATGT GTGGGGCCCC GGCGAGGGTG CTGCGCTCCC GTCCAGGTGG	180
45	TTGGGCCCAG GGCTGATCTC CCACCTGTG GAGCCTGCAT TACTGGAAGG ATCATGCGGC	240
	CAGATGATGC CAACGTGGCC GGCAATGTCC ACGGGGGGAC CATCCTGAAG ATGATCGAGG	300
50	AGGCAGGCGC CATCATCAGC ACCCGGCATT GCAACAGCCA GAACGGGGAG CGCTGTGTGG	360
	CCGCCCTGGC TCGTGTGAG CGCACCGACT TCCTGTCTCC CATGTGCATC GGTGAGGTGG	420
	CGCATGTGAG CGCGGAGATC ACCTACACCT CCAAGCACTC TGTGGAGGTG CAGGTCAACG	480
55	TGATGTCCGA AAACATCTC ACAGGTGCCA AAAAGCTGAC CAATAAGGCC ACCCTGTGGT	540
	ATGTGCCCTT GTCGCTGAAG AATGTGGACA AGTCTCTCGA GGTGCCTCCT GTTGTGTATT	600
60	CCCGGCANGA GCAGGAGGAG GAGGGCCGGA AGCGGTATGA AGCCAGAAG CTGGAGCGCA	660

	TGGAGACCAA GTGGAGGAAC GGGGACATCG TCCAGCCAGT CCTCAACCCA GAGCCGAACA	720
5	CTGTACAGTA CAGCCAGTCC AGCTTGATCC ACCTGGTGGG GCCTTCAGAC TGCACCCTGC	780
	ACGGCTTTGT GCACGGAGGT GTGACCATGA AGCTCATGGA TGAGGTCGCC GGGATCGTGG	840
	CTGCACGCCA CTGCAAGACC AACATCGTCA CAGCTTCCGT GGACGCCATT AATTTTCATG	900
10	ACAAGATCAG AAAAGGCTGC GTCATCACCA TCTCGGGACG CATGACCTTC ACGAGCAATA	960
	AGTCCATGGA GATCGAGGTG TTGGTGGACG CCGACCCTGT TGTGGACAGC TCTCAGAAGC	1020
15	GCTACCGGGC CGCCAGTGCC TTCTTCACCT ACGTGTGCTG GAGCCAGGAA GGCAGGTGCG	1080
	TGCCTGTGCC CCAGCTGGTG CCGGAGACCG AGGACGAGAA GAAGCGCTTT GAGGAAGGCA	1140
	AAGGGCGGTA CCTGCAGATG AAGGCGAAGC GACAGGGCCA CGCGGAGCCT CAGCCCTAGA	1200
20	CTCCCTCCTC CTGCCACTGG TGCTCGAGT AGCCATGGCA ACGGGCCCAG TGTCCAGTCA	1260
	CTTAGAAGTT CCCCCCTGG CCAAAAACCC AATTCACATT GAGAGCTGGT GTTGTCTGAA	1320
25	GTTTTGATAT CACAGTGTTA ACCTGTACTC TCTCCTGCAA ACCTACACAC CAAAGCTTTA	1380
	TTTATATCAT TCCAGTATCA ATGCTACACA GTGTTGTCCC GAGCGCCGGG AGGCGTTGGG	1440
	CAGAAACCCCT CGGGAATGCT TCCGAGCAGC CTGTAGGTA TGGGAAGAAC CCAGCACCAC	1500
30	TMATAAAGCT GNTGCTTGGC TGGGAAGNA	1530

35 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 997 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

45	AGGTAGTGAG AGACACATTA CACCTAACCA ACAAGAAGAA GGATCCTCCC CCTTATAATT	60
	TAACTATGTT TACAGGGAAT GCGTACATTG TGGCTTCCCG AGNATTTTCGT CCAACATGTT	120
50	TTGAAGAACC CTAAATCCCA ACAACTGATT GAATGGGTAA AAGACACTTA TAGCCCAGAT	180
	GAACACCTCT GGGCCACCCT TCAGCGTGCA CGGTGGATGC CTGGCTCTGT TCCCAACCAC	240
	CCCAAGTACG ACATCTTCAG ACATGACTTC TATTGCCAGG CTGGTCAAGT GGCAGGGTCA	300
55	TGAGGGAGAC ATCGATAAGG GTGCTCCTTA TGCTCCCTGC TCTGGAATCC ACCAGCGGGC	360
	TATCTGCGTT TATGGGGCTG GGGACTTGAA TTGGATGCTT CAAAACCATC ACCTGTTGGC	420
60	CAACAAGTTT GACCCAAAGG TAGATGATAA TGCTCTTCAG TGCTTAGAAG AATACCTACG	480

TTATAAGGCC ATCTATGGGA CTGAACTTTG AGACACACTA TGAGAGCGTT GCTACCTGTG 540
 GGGCAAGAGC ATGTACAAAC ATGCTCAGAA CTTGCTGGGA CAGTGTGGGT GGGAGACCAG 600
 5 GGCCTTGTCAA TTCGTGGCAT CCTTTAGGAT AAGAGGGCTG MTATTAGATT GTGGGTAAGT 660
 AGATCTTTTG CCTTGCAAAT TGCTGCCTGG GTGRATGCTG CTGTCTCTCT CACCCCTAAC 720
 10 CCTAGTAGTT CCTCCACTAA CTTTCTCACT AAGTGAGAAT GAGAACTGCT GTGATAGGGA 780
 GAGTGAAGGA GGGATATGTG GTAGAGCACT TGATTTCAGT TGAATGCCTG CTGGTAGCTT 840
 TTCCATTCTG TGGAGCTGCC GTTCCTAATA ATTCCAGGTT TGSTAGCGTG GAGGAGAACT 900
 15 TTGATGGAAA GAGAACCTTC CCTTCTGTAC TGTTAACCTA AAAATAAATA GCTCCTGATT 960
 CAAAGTAAGG AAAAAA AAAAGAAAAA AACTCGA 997

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(2) INFORMATION FOR SEQ ID NO: 301:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TTGAGGCCGA CGCTAGGGGC CCGGAAGRAA ACTGCGAGGC GAAGGTGACC GGGGACCGAG 60
 CATTTTCAGAT CTGCTCGGTA GACCTGGTGC ACCACCACCA TGTGCGCTGC AAGGCTGGTG 120
 35 TGTCTCCGGA CACTACCTTC TAGGGTTTTC CACCAGCTT TCACCAAGGC CTCCTCTGTT 180
 GTGAAGAATT CCATCACGAA GAATCAATGG CTGTTAACAC CTAGCAGGGA ATATGCCACC 240
 40 AAAACAAGAA TTGGGATCCG GCGTGGGAGA ACTGGCCAAG AACTCAAAGA GGCAGCATTG 300
 GAACCATCGA TGGAAAAAAT ATTTAAAATT GATCAGATGG GAAGATGGTT TGTGCTGGA 360
 GGGGCTGCTG TTGGTCTTGG AGCATTTGTC TACTATGGCT TGGACTGTC TAATGAGATT 420
 45 GGAGCTATTG AAAAGGCTGT AATTGCGCT CAGTATGTCA AGGATAGAAT TCATTCCACC 480
 TATATGTACT TAGCAGGGAG TATTGGTTTA ACAGCTTTGT CTGCCATAGC AATCAGCAGA 540
 50 ACGCCTGTTT TCATGAACTT CATGATGAGA GGCTCTTGGG TGACAATTGG TGTGACCTTT 600
 GCAGCCATGG TTGGAGCTGG AATGCTGGTA CGATCAATAC CATATGACCA GAGCCAGGC 660
 CCAAAGCATC TTGCTTGGTT GCTACATTCT GGTGTGATGG GTGCAGTGGT GGCTCCTCTG 720
 55 ACAATATTAG GGGTCTCTCT TCTCATCAGA GCTGCATGGT ACACAGCTGG CATTTGTTGG 780
 GGCCTCTCCA CTGTGGCCAT GTGTGGCCC AGTGAAAGT TTCTGAACAT GGGTGACCC 840
 60 CTGGGAGTGG GCCTGGGTCT CGTCTTTGTG TCCTCATTTG GATCTATGTT TCTTCCACCT 900

	ACCACCGTGG CTGGTGCCAC TCTTTACTCA GTGGCAATGT ACGGTGGATT AGTTCTTTTC	960
	AGCATGTTCC TTCTGTATGA TACCCAGAAA GTAATCAAGC GTGCAGAAGT ATCACCAATG	1020
5	TATGGAGTTC AAAAATATGA TCCCATTAAC TCGATGCTGA GTATCTACAT GGATACATTA	1080
	AATATATTTA TGCGAGTTGC AACTATGCTG GCAACTGGAG GCAACAGAAA GAAATGAAGT	1140
10	GACTCAGCTT CTGGCTTCTC TGCTACATCA AATATCTTGT TTAATGGGGC AGATATGCAT	1200
	TAAATAGTTT GTACAAGCAG CTTTCGTTGA AGTTTAGAAG ATAAGAAACA TGTCATCATA	1260
15	TTTAAATGTT CCGGTAATGT GATGCCTCAG GTCTGCCTTT TTTTCTGGAG AATAAATGCA	1320
	GTAATCCTCT CCCAAATAAG CACACACATT TTCAATTCTC ATGTTTGAGT GATTTTAAAA	1380
	TGTTTTGGTG AATGTGAAAA CTAAAGTTTG TGTCATGAGA ATGTAAGTCT TTTTTCTACT	1440
20	TTAAATTTA GTAGGTTTAC TGAGTAAC TAATTTAGCA AACCTGTGTT TGCATATTTT	1500
	TTTGGAGTGC AGAATATGT AATTAATGTC ATAAGTGATT TGGAGCTTGT GTAAAGGGAC	1560
	CAGAGAGAAG GAGTCACCTG CAGTCTTTTG TTTTTTTAAA TACTTAGAAC TTAGCACTTG	1620
25	TGTTATGAT TAGTGAGGAG CCAGTAAGAA ACATCTGGGT ATTTGGAAAC AAGTGGTCAT	1680
	TGTTACATTC ATCTGCTGAA CTTAACAAAA CTGTTTCATCC TGAAACAGGC ACAGGTGATG	1740
30	CATTCTCCTG CTGTTGCTTC TCAGTGCTCT CTTTCCAATA TAGATGTGGT CATGTTTGAC	1800
	TTGTACAGAA TGTTAATCAT ACAGAGAATC CTTGATGGAA TTATATATGT GTGTTTTACT	1860
	TTTGAATGTT ACAAAGGAA ATAACTTTAA AACTATTCTC AAGAGAAAAT ATTCAAAGCA	1920
35	TGAAATATGT TGCTTTTCC AGAATACAAA CAGTATACTC ATGATTGCTA AGTGTTTTTT	1980
	TATTTTTGCA TATTTATTGA ACTGTCTAAT TGAATACAGC TTGCTCTTGT CACCTCTTCA	2040
40	AGCTTTCAAG CCTTTATAGA AAAGCTTCTT TGTGGCTTAC ACTGGAAATT ATGAAAGCAG	2100
	TTTTCTCCT AAGACTTTTG GTTCTCGCA TTGCCTCTCA GACTAAGCAC TAAAAAGCAA	2160
	AGCAAAACAG AACTAGTINCT GTCTTAATGA AATATATCAA CCCAAAAGTG TAATGAGGAA	2220
45	AATGCTTCAT TAGTTTCCCC TAGCAGACTT TTAATTCTCT TACACTGCTA CACCATTACT	2280
	TTCTTGAGAC ATTTGTAAGT CCTTGATAC AGAAGAGTTA TATTTAGGAG GNCCTTAATG	2340
50	AAGGG	2345

55 (2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

5	TTTTTTTTTT TTTTTTTTTT TTTTNC AAG ATCATTGTTT ATTTATTACT TCAGATAAAA	60
	AGATAGTATA CATATTAGGG AATCCCTTAA AATTCAACTC TAGAGTTATA CACCATCTAG	120
	TACTTTTGCA ATGAATGTTA ACAACAACAA AAAAAATCTC TAAACACCTG AAAGCCCCAC	180
10	TATTAACATG GACTATGGTA ATAAAAAATT TTGACATTTA ATTTGTTCAA CATATAGTAT	240
	TTACATTATG AAACCAATGG TGATGATACA ATAAAGTGAT AAAGAAATAG TAAAAATAAA	300
15	CTTTAAAAAG CAAAGGTTTA TAGTCTGACA ATGCTAATTA TCCTAATTGT ATATAAAAAA	360
	TTAAACATA GAGCTTCTG TTACAAAATT CTTAATCCTC TGGGTGTGTA TCATTACTTG	420
	CTACCAATTT ACATGCAACA TCTGCTAGGA CTGACATTTG ATTTTITTTCC CCAAGAATGT	480
20	GTGAGTAGAT AAATGACATT TCAGAGCAGA TATTAAATTTA CTTGTGGACA GAAAAAGAAA	540
	CTCAAGATTG GTACTGGTCA CAAGCCTCTT CCAATAGAA ATTATAAAAA CAGTAAGATA	600
25	AAATTTAAAA AAAATCTAAA AAGGGGATGC ATAGGCAAAG AGTACCATAA ATGGCACAGC	660
	TCAAAAATC CCAGGACCAA TCAGACACAC ATCTTTTCTC TCTCCTTCAG CGACAAGAGG	720
	TCGATTTTGC CATCAAATAA CCATGATTGA AGCAAGCGAG GGGCACCAGG TGTACAACTG	780
30	ATTAGATCTT GCAAATACT AAGATGGGAG CAGGGGTGGC CAGAAGAAGG GGTAAATTTAT	840
	ATATAATTCA AACTATATAC AGCATAAATG GAATGCAGCC CATCCCAAAC TGGCTCTGIG	900
35	AAACAATTGG ACCTTTATAG TTAAAATTAT AACAAGTGTA ATAATACAAT AGATTTACAT	960
	GGGAAGCAAA ATCCAAGGGA CATTTTATAT TAAGTATTTA CTGTCTGTGT TCAATTTAAA	1020
	AATAATTTTG CTAAGTATAC ATCTCAACTG AAGTCTATGT AAAAAATGTC CTAATAGATA	1080
40	CAGATATTTA CCTTTGGTGA GTTGAAGGCC TTTTGTGAC TTCTGTCTGA ACTGTAGGCA	1140
	GAATGCTAGA TGTACATGCA CATATGGAGA AACTCAAGCT GAGGTCATCC AAAAGCTGTG	1200
45	CGTATGAGGA GGCTGGAGGT ACTTTGAAAG TCAAAGTAGA CCAGAAACCC AAAACAGGTA	1260
	ACAGTGAGGA TGGCAACAGG GAATGGAATG CCAATATGGC AGTAAACTTT TTTTAAAAA	1320
	CAGAAAGAGG AAGGCCTCTC GTACCAGCAG AATCCTGTAC ACGTACAAAA AAGAAAAAGC	1380
50	CACCCACCAT TTTGTAAAC AGAAGCCAAT TATAGTGTGG GAAAGTACAA ATTACAGAAA	1440
	ACCAGAAGTC AACAGAAGAA AACTACTGG TTTACTTGAG AGAAAGGAGA ATGGTTACAC	1500
55	CCGAGCAGAG TTACTTGGTG AACGCCGCCA CCACCGCCCA CAGAACCTCA TTGGTGTGG	1560
	CCTTCAGACA TTCCACTTCA GGGTCTAAGT CGAGAARNIG CCGCACTCTC TTGGTAGCCA	1620
60	AATCATACTG CTCGTCCAGA AGAGGAGCAA AAGCATTCTC CAGGACGTCC GAGGCATGAG	1680

	CCAGGTAAAT GAGGGCCAGC AAGCGCCTGT CCATGCGGTG AGGGTCATTC ACCCATTTGT	1740
	CAAGAACGGC TTCTGTACT TTCTTGATGA GCGCTGCTT AATGTTGTTA TTGGTGAGGG	1800
5	GATGTGTTGT CATGTCAAAA AGTAGGAAGT TCTGTTCTC TGTGTCAAT ACACCCCTTT	1860
	CCACCAGGTT TTTAGCTAAT CGTCCCGTA CATTTCTTAA CTGATAATGC AATTTTAATG	1920
10	GATTCATGT CTCACCACTA AGTAATTCAA TCCAGTTCTG GACCGTTTCT GGAGGCTGAG	1980
	TTTCCTTAAC ATGCTTCAGA GCTTCATCAA GAAGAACATC CCCTGTTGGA GCATCTGACT	2040
	TACAGATTAC CTTTCTGTT AATAGACTTT TAGTCTCAT TCCACAAGCC TCTAGTTGTA	2100
15	ACCTTCCTCT CAATGCTAAT TCAATTAACA TACAGCCAGC TAATCCAGAT GATATACAGT	2160
	CATTCACAAA TGATGTGTAA ACCTTCGCGG TCCTTGAGGC CCAGCAGGAG CACTTCCTCC	2220
20	ATCAGGGTCA GCCGCTTTC CTTGGAGTCG CCCTTGTCGT CGTCGTCCTG CTCGTCGCGG	2280
	CGGCTCTGCG CGTCGTCCTC GCTGCTAGCC GCGCCGCCGC CCGCCGCCCG CTCCTTGTCG	2340
	GCGGCGTTGC GGGAGGCCTC GGTCCGCG	2369
25		

(2) INFORMATION FOR SEQ ID NO: 303:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1181 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:	
	GGGACGTGTG GTTTCAGCTC GTGGCCCTCC CCGTGGGTTT GCGACGTTTA GCGACTATTG	60
40	CGCTGCGCC ACGCCGCTG CGAGACTGGG GCCGTGGYTG CTGGTCCCGG GTGATGCTAG	120
	GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG GTGTAGGTGG GAGTCACGA CCGTCCGGG	180
45	CCCGAGGTGT CCGGAAGGT GCGCACATG GCGGCAGGG GAGAGCATGG CTCAGCGGAT	240
	GGTCTGGGTG GACCTGGAGA TGACAGGATT GGACATTGAG AAGGACCAGA TTATTGAGAT	300
	GGCTGTCTG ATAACCTGACT CTGATCTCAA CATTTGGCT GAAGGTCTA ACCTGATTAT	360
50	AAAACAACCA GATGAGTTGC TGGACAGCAT GTCAGATTGG TGTAAAGAGC ATCACGGGAA	420
	GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG TACAATTACA TTGCAGCAGG CAGAGTATGA	480
55	ATTTCTGTCC TTTGTACGAC AGCAGACTCC TCCAGGCTC TGTCCACTTG CAGGAAATTC	540
	AGTTCATGAA GATAAGAAGT TTCTTGACAA ATACATGCCC CAGTTCATGA AACATCTTCA	600
	TTATAGAATA ATTGATGTGA GCACTGTTAA AGAACTGTGC AGACGCTGGT ATCCAGAAGA	660
60	ATATGAATTT GCACCAAAGA AGGCTGCTTC TCATAGGGCA CTTGATGACA TTAGTGAAAG	720

CATCAAAGAG CTTCAGTTTT ACCGAAATAA CATCTTCAAG AAAAAAATAG ATGAAAAGAA 780
 5 GAGGAAAATT ATAGAAAATG GGGAAAATGA GAAGACCGTG AGTTGATGCC AGTTATCATG 840
 CTGCCACTAC ATCGTTATCT GGAGGCAACT TCTGGTGGTT TTTTTCCTC ACGCTGATGG 900
 CTGGCAGAG CMCTTCGGTT AACTTGCATC TCCAGATTGA TTAICTCAAGC AGACAGCACA 960
 10 CGAAATACTA TTTTTCCTCT AATATGCTGT TTCCATTATG ACACAGCAGC TCCTTTGTAA 1020
 GTACCAGGTC ATGTCCATCC CTGGTACAT ATATGCATTT GCTTTTAAAC CATTTCTTTT 1080
 15 GTTTAAATAA ATAAATAAGT AAATAAGCT AGTTCTATTG AAATGCAAAA AAAAAAAAAA 1140
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA N 1181

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(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1537 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

30 CTTTTTGTGT TCCGGCCGAT CCCACCTCTC CTCGACCTG GACGTCTACC TTCCGGAGGC 60
 CCACATCTTG CCCACTCCGC GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA 120
 35 GGGACATGGC AACTACAGCG GCGCCGGCGG GCGGCGCCCG AANATGGAGC TGGCCCGGAA 180
 TGGGGAGGGT TCGAAGAAAA CATCCAGGCG GGAGGCTCAG CTGTGATTGA CATGGAGAAC 240
 40 ATGGATGATA CCTCAGGCTC TAGCTTCGAG GATATGGGTG AGCTGCATCA GCGCCTGCGC 300
 GAGGAAGAAG TAGACGCTGA TGCAGCTGAT GCAGCTGCTG CTGAAGAGGA GGATGGAGAG 360
 TTCCTGGGCA TGAAGGCTT TAAGGGACAG CTGAGCCGGC AGGTGGCAGA TCAGATGTGG 420
 45 CAGGCTGGGA AAAGACAAGC CTCCAGGGCC TTCAGCTTGT ACGCCAACAT CGACATCCTC 480
 AGACCTACTT TTGATGTGGA GCCTGCTCAG GTGCGAACAG GGCTCCTGGA GTCCATGATC 540
 CCTATCAAGA TGGTCAACTT CCCCAGAAA ATTGCAGGTG AACTCTATGG ACCTCTCATG 600
 50 CTGGTCTTCA CTCTGGTTC TATCCTACTC CATGGGATGA AGACGTCTGA CACTATTATC 660
 CGGGAGGGCA CCTGATGGG CACAGCCATT GGCACCTGCT TCGGCTACTG GCTGGGAGTC 720
 55 TCATCCTTCA TTTACTTCCT TGCCTACCTG TGCAACGCCC AGATCACCAT GCTGCAGATG 780
 TTGGCACTGC TGGGCTATGG CCTCTTTGGG CATTGCATTG TCCTGTTCAT CACCTATAAT 840
 60 ATCCACCTCC ACGCCCTCTT CTACCTCTTC TGGCTGTTGG TGGGTGGACT GTCCACACTG 900

CGCATGGTAG CAGTGTGGT GTCTCGGACC GTGGGCCCCA CACAGCGGCT GCTCCTCTGT 960
 GGCACCCCTGG CTGCCCTACA CATGCTCTTC CTGCTCTATC TGCATTTTGC CTACCACAAA 1020
 5 GTGNTAGAGG GGATCCTGGA CACACTGGAG GGCCCCAACA TCCCGCCCAT CCAGAGGGTC 1080
 CCCAGAGACA TCCCTGCCAT GCTCCCTGCT GCTGGGCTTC CCACCACCGT CCTCAACGCC 1140
 ACAGCCAAAG CTGTTGCGGT GACCCTGCAG TCACACTGAC CCCACCTGAA ATTCTTGGCC 1200
 10 AGTCCTCTTT CCCGACGTG CAGAGAGGAG GAAGACTATT AAAGGACAGT CCTGATGACA 1260
 TGTTCGTAG ATGGGGTTTG CAGCTGCCAC TGAGCTGTAG CTGCGTAAGT ACCTCCTTGN 1320
 15 AGCTGTCCGC ACTTCTGAAA GCACAAGGCC AAGAACTCCT GGCCAGGACT GCAAGGCTCT 1380
 GCAGCCAATG CAGAAAATGG GTCAGCTCCT TTGAGAACCC CTCCCCACCT ACCCCTTCCT 1440
 TCCTCTTTAT CTCTCCACA TTGTCTTGCT AAATATAGAC TTGTAATTA AAAAAAAAAA 1500
 20 AAAAAAAAAA AAAAAAAAAA AAAAAAGGG GGNCCCC 1537

25

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

35

TGCATGCCAA AACCAATGCC TGCCAAACAA AATCTTAGAC ATCCCAATAT AATATGTTAG 60
 TTATATTTCT ATTCACATCA TTATTGAAAA TACCCAGCTC AGTGCCCTGGC TTAATAAATG 120
 40 TTTAATTCCT TTACCTACTC TTGCTCTATT TTTTATTTTG AAATGGAGAT GAGCAAAATA 180
 ACACATTCAT GGCTGAAGCA ATTTTITGGA CATTTCTTGT TACCAAAAGA TCTATAATCA 240
 GGATGATCCT GAGCTGTTC AACAAGCTGT ATATAAACAG ACAATGAAAC TCTTTGCAGA 300
 45 GCTGGAAATT AAAAGGAAAG AGAGAGAAGC CAAAGAGATG CATGAAAGGA AACGACAAAG 360
 GGAAGAAGAG ATTGAAGCTC AAGAAAAAGC CAAACGGGAA AGAGAGTGGC AGAAAACTT 420
 50 TGAGGAAAGT CGAGATGGTC GTGTGGACAG CTGGCGAAAC TTCCAAGCCA ATACGAAGGG 480
 GAAGAAAGAG AAGAAAAATC GGACCTTCCT GAGACCACCG AAAGTAAAAA TGGAGCAACG 540
 TGAGTGACCG CCCAAGGTCA CAGGCACAGA ACCTTTCCTC TGCTATCTCC CTTCCTGCTT 600
 55 CGAAGGACTC ATTCTTTCCT CCCACTTCCA CCCCAACATA GAGTAGTATT TGCTTTTITAG 660
 TCCATTTTGT TTTCAATACG ATTTAATATC GATCAGAGTA ATTCTTTTGT ACATTGAAAT 720
 60 GAGGGGCTTG GTTTAAAAAA AGACCTTTC CTCTCCCTGC CCTAGAACA ACCAGTATTA 780

	GAAGGTGCCA CCATTGGTGC TGCCTTCTCT TCCCACAGCC TGTAAGTCAG TGTTTTGTAC	840
5	TTCAGTGAAT TGTGATGGTT AGAACTTTCG TGGATAGTTT GTGGAAATCA TCCAATTAAA	900
	CATACTGCTT AAAACAGTGT TGCTGTGACT TCAGAGACAA GCCTGGAAGG GGCACCTTAG	960
	GAAGCCCCCT CGCTTCAGTT GCTCGCTTCT GGGTGTGCTC CCTTGAAGG CCCAGATAAG	1020
10	ACAGGGAACA CTTGTGAGCA CACAGAGCAG CATCTGATGC OCTGTGGTGT TTGGCATGTG	1080
	CCCCCTGTCT ACTGACCAAT CAGTGTGGCA TGAGGCCAC GCCACCCAAA CCTTCACTT	1140
15	TCCAAAGAGC TAGCCGTCTT CCACCCAGTA CCATGTCTTA GCCTGTCTGC ATTTGTTAGT	1200
	GGTAATATTC TTTATGTATA ATAAATTTT ATACCCAAGC CATTGATGTA CTTTTCCTTG	1260
	TACTCTCCCT TGTGGGTCCC TTGTCTGGCT TGGCTGAACC CAAAATGCT TTGGGGTTGG	1320
20	ACAGACCTGG CTGAACCTTA GTTCTTTCAT CTATGAAATG GGAATATGAA TTACTGCAGC	1380
	AGCTTTTAGG GCAGATTGTC CATGGCATAT ACAAGGTAAC TACCATAGTG CTCCTTGGGT	1440
25	ATGCCAATA TCCTATTATT TCTGTGTAAA ATGAAGATAC TGATTGTTTT GAG	1493

30 (2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

40	AATTCGGCAG AGGNATTATA TACACTATAC TGGCATTAC TGTTTCACCC AGCCCGGAAA	60
	GTCAGAGATG TATATTGGAA AATTTACAAC TCCATCTACA TTGGTCCCA GGACGCTCTC	120
	ATAGCACATT ACCCAAGAAT CTACAACGAT GATAAGAACA CCTATATTCG TTATGAACTT	180
45	GACTATATCT TATAATTTTA TTGTTTATTT TGTGTTTAAT GCACAGCTAC TTCACACCTT	240
	AAACTTGCTT TGATTGGTG ATGTAAACTT TTAACATTG CAGATCAGTG TAGAACTGGT	300
50	CATAGAGGAA GAGCTAGAAA TCCAGTAGCA TGATTTTAA ATAACCTGTC TTTGTTTTTG	360
	ATGTTAAACA GTAAATGCCA GTAGTGACCA AGAACACAGT GATTATATAC ACTATACTGG	420
	AGGGATTICA TTTTAAATC ATCTTTATGA AGATTTAGAA CTCATTCCTT GTGTTTAAAG	480
55	GGAATGTTTA ATTGAGAAAT AAACATTTGT GWACAAAATG YTAACAAAAA AAAAAAAA	540
	AAAAAAA AAAAAAAA AAAAAAAA AACTCGA	577

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2860 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 GTGTNGACCG CTCTCNCAAT ATGGCTCCCC CGGGCTGGCA GRWRKTCRGT CWCKRGTGGC 60
 TAGCCTGTCC TGACAGGGGA GAGTTAAGCT CCCGTTCTCC ACCGTGCCCG CTGGCCAGGT 120
 15 GGGCTGAGGG TGACCGAGAG ACCAGAACCT GCTTGCTGGA GCTTAGTGCT CAGAGCTGGG 180
 GAGGGAGGTT CCGCCGCTCC TCTGCTGTCA GCGCCGGCAG CCCCTCCCGG CTTCACTTCC 240
 20 TCCCGCAGCC CTTGCTACTG AGAAGCTCCG GGATCCCAGC AGCCGCCACG CCCTGGCCTC 300
 AGCCTGCGGG GCTTCCAGTC AGGCCAACAC CGACGCGCAC TGGGGAGGAA GACAGGACCC 360
 TTGACATCTC CATCTGCACA GAGGTCTTGG CTGGAACCGA GCAGCCTCCT CCTCCTAGGA 420
 25 TGACCTCACC CTCAGCTCT CCAGTTTTC A GGTGGAGAC ATTAGATGGA GGCCAAGAAG 480
 ATGGCTCTGA GCGCGACAGA GGAAAGCTGG ATTTTGGGAG CCGGCTGCCT CCCATGGAGT 540
 30 CACAGTTCCA GGGCGAGGAC CGGAAATTCG CCCCTTCAGA TAAGAGTCAA CCTCCAACTA 600
 CCGAAAGGGA ACAGGTGCCA GTCAGCCGGA TCCAAACCGA TTTGACCGAG ATCGGCTCTT 660
 CAATCGGTC TCCCGGGGTG TCCCGAGGA TCTGGCTGGA CTTCAGAGT ACCTGAGCAA 720
 35 GACCAGCAAG TACCTCACCG ACTTCGGAAA TACACAGAGG GCTCCACAGG TAAGACGGCC 780
 TGATGAAGGC TGTGCTGAAA CCTTAAGGAC GGGGTCAATG CCTGCATCTT GCCACTGCTG 840
 40 CAGATCGACC GGGACTCTGG CAATCCTCAG CCCCTGGTAA ATGCCAGTG CACAGATGAC 900
 TATTACCGAG GCCACAGCGC TCTGCACATC GCCATTGAGA AAGAGGAGTC TGCAGTGTGT 960
 GAAGCTCCTG GTGGAGAATG GGGCCAATGT GCATGCCCGG GTCTGCGGCG ACTTCTTCCA 1020
 45 GAAGGGCCAA GGGACTTGCT TTTATTTGG TGAGCTACCC CTCTCTTTGG CCGCTTGAC 1080
 CAAGCAGTGG GATGTGGTAA GCTACCTCCT GGAGAACCCA CACCAGCCCG CCAGCCTGCA 1140
 50 GGCCACTGAC TCCAGGGCA ACACAGTCCT GCATGCCCTA GTGGATGATC TCGGACAACT 1200
 CAGCTGAGAA CATGCACTG GTGACCAGCA TGTATGATGG GCTCCTCCAA GCTKGGGSCC 1260
 SCCYTCTGCC CTACCGTGCA GCTTGAGGAC ATCCGCAACC TGCAGGATCT CACGCCTCTG 1320
 55 AAGCTGGCCG CCAAGGAGGG CAAGATCGAG ATTTTCAGGC ACATCCTGCA GCGGGAGTTT 1380
 TCAGGACTGA GCCACCTTTC CGAAAGTTC ACCGAGTGGT GCTATGGGCC TGTCCGGGTG 1440
 60 TCGCTGTATG ACCTGGCTTC TGTGGACAGC TGTGAGGAGA ACTCAGTGCT GGAGATCATT 1500

GCCTTTCATT GCAAGAGCCC GCACCGACAC CGAATGGTGC TTTTGGAGCC CCTGAACAAA 1560
 5 CTGCTGCAGG CGAAATGGGA TCTGCTCATC CCCAAGTTCT TCTTAAACTT CCTGTGTAAT 1620
 CTGATCTACA TGTTTCATCTT CACCGCTGTT GCCTACCATC AGCCTACCTT GAAGAAGCAG 1680
 GCGGCCCTC ACCTGAAAGC GGAGGTGGA AACTCCATGC TGCTGACGGG CCACATCCTT 1740
 10 ATCTGCTAG GGGGATCTA CCTCCTCGTG GGGCCAGCTG TGGTACTTCT GCGGCGCCA 1800
 CGTGTTCATC TGGATCTCGT TCATAGACAG CTACTTTGGA AATCCTCTTC CTGTTCCAGG 1860
 CCTGCTTCA CAGTGGTGTG CCAGGTGCTG TGTTCCTGG GCCATCGAGT GGTACCTGCC 1920
 15 CCTGCTTGTG TCTGCGCTGG TGGCTGGGCT GGCTGAACCT GCTTTACTAA TACACGTGGC 1980
 GTTCCAGCAC ACAGGCAGTC TACAGTTTCA TGWTCCCTGA AGCCTGGTG AGCCTGAGCC 2040
 20 AGGAGGCTTG GCGCCCGAA GCTCCTACAG GCCCCAATGC CACAGAGTCA GTGCAGCCCA 2100
 TGGAGGGACA GGAGGACGAG GGCAACGGGG CCCAGTACAG GGGTATCCTG GAAGCCTCCT 2160
 TGGAGCTCTT CAAATTCACC ATCGGCATGG GCGAGCTGGC CTTCAGGAG CAGCTGCACT 2220
 25 TCCGCGGCAT GGTGCTGCTG CTGCTGCTGG CCTACGTGCT GCTCACCTAC ATCCTGCTGC 2280
 TCAACATGCT CATCGCCCTC ATGAAGCGAA CGTCACAGTG TCGCCACTGA CAGCTGGAGC 2340
 30 ATCTGGAAGC TGCAGAAAGC CATCTCTGTC CTGGAGATGG AGAATGGCTA TTGGTGGTGC 2400
 AGGAAAAAGC AGCGGGCAGG TGTGATGCTG ACCGTTGGCA CTAAGCCCAG ATGGCAGCCC 2460
 CGATGAGCGC TGGTGCTTCA GGGTGGAGGA GGTGAAGTGG GCTTCATGGG GAGCAGACGC 2520
 35 TGCCTACGCT GTGTGAGGAC CCGTCAGGGG CAGGTGTCCC TCGAACTCTC GAGAACCTG 2580
 TCCTGGCTTC CCTCCCAAG GAGGATGAGG ATGGTGCCTC TGAGGAAAAC TATGTGCCCG 2640
 40 TCCAGCTCCT CCAGTCCAAC TGATGGCCCA GATGCAGCAG GAGGCCAGAG GACAGAGCAG 2700
 AGGATCTTTC CAACCACATC TGCTGGCTCT GGGGTCCCAG TGAATTCTGG TGGCAAATAT 2760
 45 ATATTTTCAC TAACTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAVGAGGG GGGGCCCGKT 2820
 ASCCAAWTTC GCCCTATAAG TGAGTGCCWA TTACGATAAA 2860

50

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

	CTGCTTGTGT CTGCGCTGGT GCTGGGCTGG CTGAACCTGC TTTACTATAC ACGTGGCTTC	60
	CAGCACACAG GCATCTACAG TGTCTGATC CAGAAGCCCT GGTGAGCCTG AGCCAGGANN	120
5	TTGGCGCCCC GAAGCTCCTA CAGGCCCAA TGCCACAGAG TCAGTGCAGC CCATGGAGGG	180
	ACAGGAGGAC GAGGGCAACG GGGCCAGTA CAGGGGTATC CTGGAAGCCT CTTGGAGCT	240
10	CTTCAAATTC ACCATCGGCA TGGGCGAGCT GGCCTTCCAG GAGCAGCTGC ACTTCCGCGG	300
	CATGGTGCTG CTGCTGCTGC TGGCCTACGT GCTGCTCACC TACATCCTGC TGCTCAACAT	360
	GCTCATGCGC CTCATGNAGC GAGACGWCA ACAGTGTGCG CACTGACAGC TGGAGCATCT	420
15	GGAAGCTGCA GAAAGCCATC TCTGTCTGG AGATGGAGAA TGGCTATTGG TGGTGCAGGA	480
	AGAAGCAGCG GGCAGGTGTG ATGCTGACCG TTGGCACTAA GCCAGATGGC AGCCCCGATG	540
20	AGCGCTGGTG CTTCAGGGTG GAGGAGGTGA ACTGGGCTTC ATGGGAGCAG ACGCTGCCTA	600
	CGCTGTGTGA GGACCCGTCA GGGGAGGTG TCCCTCGAAC TCTCGAGAAC CCTGTCTCTG	660
	CTTCCCTCC CAAGGAGGAT GAGGATGGT CCTCTGAGGA AAATATGTG CCGTCCAGC	720
25	TCCTCCAGTC CAACTGATGG CCCAGATGCA GCAGGAGGCC AGAGGACAGA GCAGAGGATC	780
	TTTCCAACCA CATCTGCTGG CTCTGGGTC CCAGTGAATT CTGGTGGCAA ATATATATTT	840
30	TCACTAAMWM AAAAAAAAAA AAAAAAAAAA ACTGGA	876

35 (2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

45	CATGACCCGC CTGATGCGAT CCGCACAGC CTCTGGTTCC AGCGTCACTT CTCTGGATGG	60
	CACCCGCAGC CGTCCCACA CCAGCGAGGG CACCCGAAGC CGTCCCACA CCAGCGAGGG	120
	CACCCGCAGC CGTCCGACA CCAGCGAGGG GGCCACCTG GACATCACCC CCAACTCGGG	180
50	TGCTGCTGGG AACAGGCCG GCCCAAGTCC ATGGAGGTCT CCTGCTAGGC GGCTGCCCA	240
	GCTGCCGCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC CTCCCCGGCC CTTTTCGCC	300
55	CCCTGCCTGC CATACTGCGC CTAAGTGGT ATTAATCCAA AGCTTATTTT GTAAGAGTGA	360
	GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC TCTCCAAAGG CGGGGTGGCG	420
	GTGACCAAAA GGAAGGAAGC AAGCATCTCC GCATCGCATC CTCTTCCATT AACCAGTGGC	480
60	CGGTGGCCAC TCTCTCCCC TCCTCAGAG ACACAAACT GCCAAAACA AGACGCGTAC	540

	AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCTGAGC ATCCTGGTTC AAACGGGTGC	600
5	CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTCTCTCTT AACTGAGGAG AAGCTGATCC	660
	AGTTTCCGGA AACAAAATCC TTTTCTCAT TGGGAGGGG GGTAAATAGT ACATGCAGGC	720
	ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGGTG GGATTCATGT CGAGGCTAGA	780
10	GGCATTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA ACCGATTTT AAAGTTGGT	840
	CATCTAGAAA GCTTTGAATG CAGAAGCAA CAAGCTTGAT TTTCTAGCA TCCTCTTAAT	900
15	GTGCAGCAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG AAAAAATAT TTCAGCAAAC	960
	GTGGGCATC ATGGTTTGTG AAGGCTTTAG TTCTGCTTC TGCCTCTCCT CCACAGCCCC	1020
	AACCTCCAC CCCTGATACA TGAGCCAGT ATTATTCTTG TTCAGGGAGA AGATCATTTA	1080
20	GATTTGT TTTT GCATTCTTA GAATGGAGG CAACATTCCA CAGCTGCCCT GGCTGTGATG	1140
	AGTGTCTTG CAGGGGCCG AGTAGGAGCA CTGGGGTGG GCGGAATG GGGTTACTCG	1200
25	ATGTAAGGA TTCCTGTG TGTGTGTGAG ATCCAGTGCA GTTGTGATT CTGTGGATCC	1260
	CAGCTTGGT CCAGGAATTT TGTGTGATT GCTTAAATCC AGTTTCAAT CTTCGACAGC	1320
	TGGGCTGGA CGTGAATCA GTAGCTGAAC CTGTCTGACC CGGTACGTT CTGGATCCT	1380
30	CAGAACTCT TGCTCTGTC GGGGTGGGG TGGGAATCA CGTGGGAGC GTGGCTGAG	1440
	AAAATGTAAG GATTCTGGA TACATATTCC ATGGGACTTT CCTTCCCTCT CTGCTTCCT	1500
35	CTTTCTCTG TCCCTAACCT TTCGCCGAAT GGGGCAGCAC CACTGACGTT TCTGGGCGGC	1560
	CAGTGGGCT GCCAGGTCC TGTACTACT CCTGTACTT TTCATTTTGG CTCACCGTGG	1620
	ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT GTAAGTCAGC CACTGGGACC	1680
40	CGAGGATTC TGGGACCCG CAGTTGGGAG GAGGAAGTAG TCCAGCCTTC CAGGTGGCGT	1740
	GAGAGGCAAT GACTCGTTAC CTGCCGCCA TCACCTTGA GCCTTCCCT GGCTTGAGT	1800
45	AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGA TGGGAACTA TTGTGCACAA	1860
	GTCTTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA TTTCAGACC AATAAATTTG	1920
	TAACTTTGCA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAATC	1980
50	GAGGGGGGCC CGTACCCAAT TCGCGTATA TGATCGTAAA CAATC	2025

55 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3026 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

5	TAGGCAGCAC TGAAATATCC TAACCCCTA AGCTCCAGGT GCCCTGTGGN ACGAGCAACT	60
	GGACTATAGC AGGGCTGGGC TCTGTCTTCC TGGTCATAGG CTCACTCTTT CCCCCAAATC	120
	TTCTCTGGA GCTTTGCAGC CAAGGTGCTA AAAGGAATAG GTAGGAGACC TCTTCTATCT	180
10	AATCCTTAAA AGCATAATGT TGAACATTCA TTCAACAGCT GATGCCCTAT AACCCCTGCC	240
	TGGATTCTT CCTATTAGGC TATAAGAAGT AGCAAGATCT TTACATAATT CAGAGTGGTT	300
15	TCATTGCCTT CCTACCTCT CTAATGGCCC CTCCATTTAT TTGACTAAAG CATCACACAG	360
	TGGCACTAGC ATTATACCAA GAGTATGAGA AATACAGTGC TTTATGGCTC TAACATTACT	420
	GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG GATGGCAGCC TCAGGGCTTC CTTATGTCTT	480
20	CCACCACAAG AGCTCCTTGA TGAAGGTCAT CTTTTCCTCC TATCCTGTTC TTCCCTTCCC	540
	CGCTCCTAAT GGTACGTGGG TACCCAGGCT GGTCTTGGG CTAGGTAGTG GGGACCAAGT	600
25	TCATTACCTC CCTATCAGTT CTAGCATAGT AAACACGGT ACCAGTGTTA GTGGGAAGAG	660
	CTGGGTTTTC CTAGTATACC CACTGCATCC TACTCCTACC TGGTCAACCC GCTGCTTCCA	720
	GGTATGGGAC CTGCTAAGTG TGAATTACC TGATAAGGGA GAGGGAATA CAAGGAGGGC	780
30	CTCTGGTGTT CCTGGCCTCA GCCAGCTGCC CACAAGCCAT AAACCAATAA AACAAGAATA	840
	CTGAGTCAGT TTTTATCTG GGTCTCTTC ATTCCCACTG CACTTGGTGC TGCTTTGGCT	900
35	GACTGGGAAC ACCCCATAAC TACAGAGTCT GACAGGAAGA CTGGAGACTG TCCACTTCTA	960
	GCTCGGAAT TACTGTGTAA ATAACTTTC AGAACTGCTA CCATGAAGTG AAAATGCCAC	1020
	ATTTTGCTTT ATAATTCTA CCCATGTTGG GAAAACTGG CTTTTCCTCA GOCCTTTCCA	1080
40	GGGCATAAAA CTCAACCCCT TCGATAGCAA GTCCCATCAG CCTATTATTT TTTTAAAGAA	1140
	AACTTGCAT TGTTTTCTT TTTACAGTTA CTTCCTTCTT GCCCCAAAAT TATAAACTCT	1200
45	AAGTGTAATA AAAAGTCTTA ACAACAGCTT CTGCTTGTA AAAATATGTA TTATACATCT	1260
	GTATTTTAA ATTCTGCTCC TGAAAAATGA CTGTCCCAT TCCACTCAC TGCATTGGG	1320
	GCCTTTCCCA TTGGTCTGCA TGTCTTTTAT CATTCAGGC CAGTGGACAG AGGGAGAAGG	1380
50	GAGAACAGGG GTCGCCAACA CTTGTGTGCT TTTCTGACTG ATCCTGAACA AGAAAGAGTA	1440
	ACACTGAGGC GCTGCTCCC ATGCACAACT CTCCAAAACA CTTATCCTCC TGCAAGAGTG	1500
55	GGCTTTCCAG GGTCTTTACT GGAAGCAGT TAAGCCCCCT CCTCACCCTT TCCTTTTTC	1560
	TTTCTTTACT CCTTTGGCTT CAAAGGATTT TGGAAAAGAA ACAATATGCT TTACTCAT	1620
60	TTTCAATTTT TAAATTTGCA GGGGATACTG AAAAATACGG CAGGTGGCCT AAGGCTGCTG	1680

TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT TACAAGATAA AAAACGAATC CCCTAAACAA 1740
AAAGAACAAT AGAACTGGTC TTCCATTTTG CCACCTTTCC TGTTTCATGAC AGCTACTAAC 1800
5 CTGGAGACAG TAACATTTCA TTAACCAAAG AAAGTGGGTC ACCTGACCTC TGAAGAGCTG 1860
AGTACTCAGG CCACTCCAAT CACCCTACAA GATGCCAAGG AGGTCCCAGG AAGTCCAGCT 1920
CCTTAAACTG ACGCTAGNMA ATAAACCTGG GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT 1980
10 CCATCTGTGA GGTGAYAGGC AAGGATGAAA GACAAAGAAG GAAAAGAGTA TCAAAGGCAG 2040
AAAGGAGATC ATTTAGTTGG GTCTGAAAGG AAAAGTCITT GCTATCCGAC ATGTACTGCT 2100
15 AGTACCTGTA AGCATTTTAG GTCCAGAAT GGAAAAAAA ATCAGCTATT GGTAATATAA 2160
TAATGTCCTT TCCCTGGAGT CAGTTTTTTT AAAAGTTAA CTCTTAGTTT TTACTTGTGT 2220
AATTCTAAAA GAGAAGGGAG CTGAGGCCAT TCCCTGTAGG AGTAAAGATA AAAGGATAGG 2280
20 AAAAGATTCA AAGCTCTAAT AGAGTCACAG CTTTCCCAGG TATAAACCT AAAATTAAGA 2340
AGTACAATAA GCAGAGGTGG AAAATGATCT AGTTCTTGAT AGCTACCCAC AGAGCAAGTG 2400
25 ATTTATAAAT TTGAAATCCA AACTACTTTC TTAATATCAC TTGGTCTCC ATTTTCCCA 2460
GGACAGGAAA TATGTCCCC CCTAATTTC TTGCTTCAAA AATTAAAAATC CAGCATCCCA 2520
AGATCATTTCT ACAAGTAATT TTGCACAGAC ATCTCCTCAC CCCAGTGCCT GTCTGGAGCT 2580
30 CACCCAAGGT CANCCAAACA ACTTGGTTGT GAACCCAACT GCCTTAACCT TCTGGGGGAG 2640
GGGGATTAGC TAGACTAGGA GACCAGAAG TGAATGGGAA AGGGTGAGGA CTTCACAATG 2700
35 TTGGCCTGTC AGAGCTTGAT TAGAAGCCAA GACAGTGCCA GCAAAGGAAG ACTTGGCCCA 2760
GGAAAAACCT GTGGGTGTG CTAATTTCTG TCCAGAAAAT AGGGTGACA GAAGCTTGTG 2820
GGGTGCATGG AGGAATTGGG ACCTGGTTAT GTTGTATTTC TCGGACTGTG AATTTTGGTG 2880
40 ATGTAAACA GAATATTCTG TAAACCTAAT GTCTGTATAA ATAATGAGCG TTAACACAGT 2940
AAAATATTCA ATAAGAAGTC AAAAAAAAAA AAAAAAACT CGAGGGGGG CCCGGTACCC 3000
45 AATTTNCCAA ATAGAGATNG TATTAC 3026

50 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

60 GCAGGCTTTG TGCTCACCTA CAAGCTGGGT GAGCAGGGTG CCAGCAGCCT GTTCCTCTT 60

CTCTGCTGG ACCACGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG TGTGGGTGCT 120
 GTGGTCTGCT CCATCGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA GCACTGGAAA 180
 5 CTGCTGCCTC TGTGARGTC GGTGCTGCGC TTCCGCCTCG GGGCCTAGC CTGTCAGACT 240
 GCCTTGGTCT TCCACCTGGA CACCCTGGG GCCAGCATGG ACGCTGGCAC AATCTTGAGA 300
 10 GGGTCAGCCT TGCTGAGCCT ATGCTGTCAG CACTTCTTGG GAGGCCTGGT CACCACAGTC 360
 ACCTTCACTG GGATGATGCG CTGCAGCCAG CTGGCCCCA GGGCCTGAG GCCACACACT 420
 ACAGCCTTCT GGCCACGCTG GAGCTGCTGG GGAAGCTGCT GCTGGGCACT CTGCGGAGGC 480
 15 CTGGCTGATG GGTGGGGCC ACATCCCTGC TTCTTGCTCC TGCTCATCCT CTCTGCCTTT 540
 CCGTTCCTGT ACCTGGACCT AGCACCAGC ACCTTTCCTT GAGCTGAGTG GCTGGAGTGG 600
 20 TCAATAAAGC CACATGTGCC TGTGGCCCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 660
 AACTGGAGGG GGGGCCCGGT ACCCAAATCG CCGGATATGA TCGTAAACAA TC 712

25

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CAAATTTCA GAACTTTCAG GAGGCAAGA GAATATCAA CAAAGATTTC TGGAAGTATT 60
 TTGCCAACCT TCTGGTTGAG CTGCAAGAAA ATATTTATGG TGAGAACTTT TCTGTTTCCC 120
 40 GTTATGGGT TTTTGGTTGG TTTTGTGTTG TTTTITACTA TGCTTTGGTC TGTA AAAATA 180
 TGCAACTGAA CTACATTCAG AAGGAAATAT TGCTACATA GAATATTATA TGAAGTTGGT 240
 45 ACATAATTCT GATGAGGAAA AAAATCTTT GCAATTCCTT AAGCCATATT GTTGTTTTTT 300
 TGTGTGTTT TCCCTGGATG AAAATATCAG TATTAAGTAG ACAGCATATT ATTCAAGTGT 360
 TTAGACTTAT TAATATGTTT TTGCTCTGTA TTTATACATA TGTGTATTTT GGAAAGTATT 420
 50 GCCTTTTTTA AGGGAAGCTA TAATTCGATA CATAGTGAAA AAGGAATGG TGACCCCTTT 480
 GTGCCTCTTC CACTGAGGAT AACAAACAGC ATTGTAATCC ATTCTCTTGC ACCTTCTTCT 540
 55 TCTTATCTTG TTATTACGGT TTTATTAATT TTGTAGAGGG ACAGGGAGTG GGCAAGGGGA 600
 AGAAGCAGCT TATTTGACTA ACCAGCCCTT CTGTGGTCCA CCAGCGTCTT GGCTTGGTGG 660
 GAGGGCTCTC AATCAGCAGG GCCCCAGGAG GGAAGAAGAA GTGGGGCAA GCCTGGCCTC 720
 60

GCGCTCGGG AGCTTTGCCA TCTGAGCCAC GCGTCCTCCA GGCCATGCTC CTTGAACTTG 780
 GAAATGTCAA CCGGAGCCCT TACACCAGCC CTCCAGCATC TAATAGACTT GAATCTACTC 840
 5 TAAACGAATA TTTAATCCAA CCTCACTACA TTGTAGCTCA GTCCAACGAC TAACCCTGAA 900
 ATGGGGGTGT TCCAGCCTTC AGCGAGATGG CCAAGCGGTC CCCTGGGGGC TGTGGCAGCG 960
 GGCTTATCCT TCTCTGTTGC CAACCTTGCC GTCCGACCTC CTCGGCCCCC ATGCGGTGAC 1020
 10 CCCGTCGGTG TCTGTGTCTG TCCATACGTG TGAGTCCAGC TAAAAAGACA AAACAGAACC 1080
 CGTGGGCCCA GCTCGGAAGG TCGTGGAGA AGGCTCCGAC GTCTCCGAAG TGCAGCCCTT 1140
 15 GGGATGGCAT TCCGTTGTGT GCCTTATTCC TGGAGAATCT GTATACGGCT CGCCTATAGA 1200
 AATATAGCCT CTCATGCTG TATTAAAAGG ACTTTTAAAA GCAAAAAAAAA AAAAAAAAAA 1260
 CTTGAGGGGG GGNCCGGTAC CCAATTNTC 1289
 20

(2) INFORMATION FOR SEQ ID NO: 313:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Ile Leu Phe Ser Ser Ser
 1 5 10 15

35

Leu Pro Phe Leu Trp Leu
 20

40

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Met Phe Leu Thr Gln Gly Gly Pro Leu Pro Ser Thr Arg Ala Arg
 1 5 10 15

50

Pro Thr Cys Gln Ala Gly Ala Leu Pro Lys Pro Ser Gly Leu Leu Gly
 20 25 30

55

Val Thr Cys Trp Asn Gly Leu Lys Gly Pro Leu Cys Gly Asn Arg Cys
 35 40 45

Ser Pro Asn Thr Leu Leu Leu Ala Ala Arg Gln Ala Leu Trp Lys Gly
 50 55 60

60

Arg Gly Arg Thr His Gln Asp Leu Pro Gly Pro Leu Gln Gly Arg Gln

546

	65					70						75					80
	Leu	Gly	Pro	Glu	Pro	Lys	His	Leu	Ala	Leu	Leu	Pro	Pro	Arg	Gly	Gln	
					85					90					95		
5																	
	Glu	Ala	Ser	Trp	Ala	Ser	Ser	Leu	Pro	Gly	Gln	Gly	Pro	Leu	Pro	Leu	
					100				105					110			
10																	
	Pro	His	Ile	Asn	Cys	Thr	Val	Phe	Ser	Leu	Lys	Ala	Ser	Phe	Ile	Lys	
					115			120					125				

15

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:-
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

25 Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15
Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 316:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40 Met Asp Gly Phe Ser Ser Arg Leu Phe Ser Ser Leu Pro Phe Val Ala
1 5 10 15

45 Leu Gln Trp Phe Ile Val Ile Ser His Leu Leu Ser Leu Ser Leu Ser
20 25 30

Ala Cys Cys Tyr Gln Thr His Cys Ser Leu Xaa Gln Leu Ser Ser Ala
35 40 45

50 Phe Ser Xaa Met Gly Glu Ser Cys Val Gly Glu Arg Glu Tyr Xaa Phe
50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 317:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

5

Met Pro Leu Ile Asn Leu Leu Leu Tyr Tyr Val Pro Asn Gly Gly
 1 5 10 15

10

Lys Gln Asp Lys Lys
 20

(2) INFORMATION FOR SEQ ID NO: 318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Gly Arg His Leu Val Leu Val Met Phe Ile Thr Thr Ser Leu His
 1 5 10 15

25

Ser Gly Thr Pro Val Pro Glu Asn Val Ile Cys Gly Val Thr Lys Gly
 20 25 30

Pro Gln Gly Lys Lys Lys Lys
 35

30

(2) INFORMATION FOR SEQ ID NO: 319:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Trp Trp Ser Arg Asp Tyr Thr Met Val Phe Leu Leu Phe Thr
 1 5 10 15

45

Met Val Phe Thr Gly Asp Leu Val Ile Arg Gly Arg Thr Glu Leu Ser
 20 25 30

Leu

50

(2) INFORMATION FOR SEQ ID NO: 320:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

60

Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe

548

1 5 10 15
 Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu Ile Leu
 20 25 30
 5 Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu Leu Pro
 35 40 45
 10 Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala Glu Asn
 50 55 60
 Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val
 65 70 75 80
 15 Gln Thr Ser Glu Pro Ser Gly Thr
 85

20 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Gln Pro Gly Ala Gly Val Leu Val Leu Gly Leu Leu Leu Pro Pro
 1 5 10 15
 30 Pro Gln Ser Pro Ser Leu Ser
 20

35 (2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Thr Phe Thr Leu Gly Asp Ser Gln Val Leu Leu Ile Asn Leu Phe
 1 5 10 15
 45 Pro Ser Met Pro Ser Gly Ser Cys Ala Arg Pro
 20 25

50 (2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

60 Met Cys Leu Glu Cys Trp Ala Glu Asn Leu Gly Pro His His Thr Ser

1 5 10 15

Ser Leu Leu Asn Pro Arg His Leu Pro Ser Ile Pro Ala Met Phe Pro
 20 25 30

5 Val Ser Ser Gly Cys Phe Gln Glu Gln Glu Met Asn Lys Ser Leu
 35 40 45

10 Val Ser Cys Leu Phe Val Leu His Phe Val Leu His Cys Ile Phe Xaa
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 324:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

25 Met Leu Ser Thr Ser Glu Tyr Ser Gln Ser Pro Lys Met Glu Ser Leu
 1 5 10 15

Ser Ser His Arg Ile Asp Glu Asp Gly Glu Asn Thr Gln Ile Glu Asp
 20 25 30

30 Thr Glu Pro Met Ser Pro Val Leu Asn Ser Lys Phe Val Pro Ala Glu
 35 40 45

35 Asn Asp Ser Ile Leu Met Asn Pro Ala Gln Asp Gly Glu Val Gln Leu
 50 55 60

Ser Gln Asn Asp Asp Lys Thr Lys Gly Asp Asp Thr Asp Thr Arg Asp
 65 70 75 80

40 Asp Ile Ser Ile Leu Ala Thr Gly Cys Lys Gly Arg Glu Glu Thr Val
 85 90 95

Ala Glu Glu Val Cys Ile Asp Leu Thr Cys Asp Ser Gly Ser Gln Ala
 100 105 110

45 Val Pro Ser Pro Ala Thr Arg Ser Glu Ala Leu Ser Ser Val Leu Asp
 115 120 125

50 Gln Glu Glu Ala Met Glu Ile Lys Glu His His Pro Glu Glu Gly Ser
 130 135 140

Ser Gly Ser Glu Val Glu Glu Ile Pro Glu Thr Pro Cys Glu Ser Gln
 145 150 155 160

55 Gly Glu Glu Leu Lys Glu Glu Asn Met Glu Ser Val Pro Leu His Leu
 165 170 175

Ser Leu Thr Glu Thr Gln Ser Gln Gly Leu Cys Leu Arg Arg His Pro
 180 185 190

60

Lys Lys Lys Lys
195

5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

15 Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
1 5 10 15

Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20 25 30

20 Ala Xaa Xaa Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
35 40 45

Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr
50 55 60

25 Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val
65 70 75 80

30 Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val
85 90 95

Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys
100 105 110

35 Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp
115 120 125

Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln
130 135 140

40 Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala
145 150 155 160

45 Ala Arg Xaa His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg
165 170 175

Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met
180 185 190

50 Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn
195 200 205

Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala
210 215 220

55 Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro
225 230 235 240

60 Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
245 250

5 (2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15

15 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
 20 25 30

Val Ile Lys Asn Asn Ser His Tyr Gln Thr Ser Lys Ala Leu Glu Leu
 35 40 45

20 Glu Lys Thr Thr Glu Asn Lys Glu Ser Asn Pro Phe Ile Leu Gln Val
 50 55 60

Asn Lys Leu Xaa
 65

30 (2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Gly Glu Gly Lys Asn Gly Phe Gly Gly Phe Val His Thr Ala Asp
 1 5 10 15

40 Ala Cys Trp Glu Gly Val His Ser Glu Pro Val Cys Arg Thr Val His
 20 25 30

Thr Val His Thr Cys His His Gln Ala Phe Leu Val Leu Ile Gly Trp
 35 40 45

45 Ser Lys Ser Gly Lys Glu Arg Lys Glu Ala Phe Leu Thr Ala Ile Ile
 50 55 60

50 Leu Asn Ser Arg Ser Ile His Ile Ser Cys Ser Trp Pro Pro Ser Pro
 65 70 75 80

Val Pro Gln Xaa

55 (2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

5 Met Leu Leu Ile Asn Leu Leu Trp Leu Val Thr Met Ile Lys Ser Val
 1 5 10 15
 Ile Asn Asn Asn Ile Ile Leu Phe Leu Lys Lys Lys Ser Leu Phe Phe
 20 25 30
 10 Ile Asp Ser Val
 35

15

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

25 Met Thr Phe Pro Phe Glu Lys Lys Ile Val Ala Phe Ser Ala Phe Tyr
 1 5 10 15
 Leu Ile Pro Gly Glu Ser Arg Leu Ala Pro Thr Phe Asn Pro Ser Ala
 20 25 30
 30 Asp Met Thr Val Ile Leu Arg Gly Arg Ala Gln His Lys Thr Ala Met
 35 40 45
 Leu Glu Ser Tyr Asn Trp Lys Val Ser Cys Gln Leu Arg Glu Xaa
 50 55 60
 35

(2) INFORMATION FOR SEQ ID NO: 330:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

45

Met His Ser Lys Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile
 1 5 10 15
 Leu Ile Leu Pro Val Cys Ala His Leu His Glu Glu Leu Asn Cys Cys
 20 25 30
 Phe His Arg
 35
 55

(2) INFORMATION FOR SEQ ID NO: 331:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Gly Ala Leu Val Leu Leu Leu Cys Leu Leu Val Gly Val Gln Gln
 1 5 10 15
 Ser Gly Ser Val Trp Asp Ser
 20

10

(2) INFORMATION FOR SEQ ID NO: 332:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

20

Met Gln Ser Ala Glu Ile Leu Ser Trp Thr Asp Val Leu His Asp Phe
 1 5 10 15

25

Leu Phe Ser Leu Phe Leu Trp Pro Ala Phe Glu Asp Arg Ala Leu Leu
 20 25 30

Ile Phe Thr Leu Asn Gln Ile Val
 35 40

30

(2) INFORMATION FOR SEQ ID NO: 333:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

40 Met Gln Ser Leu Val Gln Trp Gly Leu Asp Ser Tyr Asp Tyr Leu Gln
 1 5 10 15

Asn Ala Pro Pro Gly Phe Phe Pro Arg Leu Gly Val Ile Gly Phe Ala
 20 25 30

45

Gly Leu Ile Gly Leu Leu Leu Ala Arg Gly Ser Lys Ile Lys Lys Leu
 35 40 45

50

Val Tyr Pro Pro Gly Phe Met Gly Leu Ala Ala Ser Leu Tyr Tyr Pro
 50 55 60

Gln Gln Ala Ile Val Phe Ala Gln Val Ser Gly Glu Arg Leu Tyr Asp
 65 70 75 80

55

Trp Gly Leu Arg Gly Tyr Ile Val Ile Glu Asp Leu Trp Lys Glu Asn
 85 90 95

Phe Gln Lys Pro Gly Asn Val Lys Asn Ser Pro Gly Thr Lys Xaa
 100 105 110

60

(2) INFORMATION FOR SEQ ID NO: 334:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Ala Pro Ser Leu Leu Leu Leu Ala Pro Leu Cys Ser Leu Glu Ala
 1 5 10 15

Val Leu Ser Ser Pro Leu Glu Lys Gln Cys Gln Leu Pro Gly Ile Phe
 15 20 25 30

Cys Gln Leu Gln Leu Pro Cys Pro Leu Leu Leu Ser Ala Gln Leu Leu
 35 40 45

20 Lys Gly Ile Val Xaa Pro Arg Cys Pro Ala Ser Leu Pro Gln Pro Pro
 50 55 60

His Pro Ala Pro Ser Trp His Leu Pro Leu His Cys Thr Glu Arg Xaa
 65 70 75 80

25 Pro His His Leu Pro Leu Gln Gly Gly Ser Ser Asn Met Glu Glu Xaa
 85 90 95

30 Asn Tyr Arg Gly Tyr Xaa Asp Ala Gln Leu
 100 105

(2) INFORMATION FOR SEQ ID NO: 335:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Thr Thr Cys Leu Phe Gly Leu Leu Ser Cys Glu Met Ser Ala Gln
 1 5 10 15

45 Val Ser Gln Lys Ser Cys Val Tyr Asp Glu Ser Glu Cys Phe Ser Ser
 20 25 30

Val Gly Gln Leu Leu Ala Leu Leu Ile Leu Val Tyr Val Leu Pro Ser
 35 40 45

50 Ile Xaa
 50

(2) INFORMATION FOR SEQ ID NO: 336:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid

60

555

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

5 Met Leu Trp Lys Cys Ser Gln Asn Ile Ala Arg Cys Leu Leu Leu Leu
 1 5 10 15

Leu Ala Leu Val Glu Ile Lys Leu Glu Asp Leu Gln Ser Gln Leu His
 20 25 30

10 Pro Thr Trp Lys Ser Ile Pro Gly Pro Ser Pro Arg Asn Gln His Arg
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 337:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

25 Met Leu Ile Pro Leu Gln Cys Leu Phe Ser Ser Asp Arg Met Leu Thr
 1 5 10 15

30 Phe Leu Thr Pro Trp Gln Lys Gly Glu Lys Cys Val Leu Gly Trp Val
 20 25 30

Thr Lys Phe Leu Ser Glu Ile Ser Xaa
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 338:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

45 Met Thr Phe Ser Ser Leu Lys Leu Phe Val Leu Thr Cys Ile Ile Lys
 1 5 10 15

Gly Leu Glu Arg Phe Ile Ile Leu Arg Glu Val Cys Asn Gln Glu Ile
 20 25 30

50 Gln Arg Ser Leu Ser Ser Asn Leu Val His Val Leu Leu Gln Pro Ala
 35 40 45

55 Thr Phe Lys Asp Val Leu Val Thr Glu Ile Ile Cys Leu Cys Met Cys
 50 55 60

Leu Tyr Ser Ile Lys Tyr Met Pro Pro Gln Lys Lys
 65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

5
 10 Lys Val Tyr Ile Phe Leu Ile Phe Met Val Leu Ile Leu Pro Ser Leu
 1 5 10 15
 Gly Leu Thr Arg Tyr Met Pro Pro Xaa Ser Xaa Leu Asn Ser Glu
 20 25 30
 15

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

20
 25 Met Ala Lys Ile Ser Pro Phe Glu Val Val Lys Arg Thr Ser Val Pro
 1 5 10 15
 Val Leu Val Gly Leu Val Ile Val Ile Val Ala Thr Glu Leu Met Val
 30 20 25 30
 Pro Gly Thr Ala Ala Ala Val Thr Gly Lys
 35 40
 35

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

40
 45 Met Arg Leu Phe Phe Ile Gly Phe Leu Leu Leu Phe Ser Phe Gly Leu
 1 5 10 15
 Leu Arg Gln Pro Ser Leu Ser Ala Glu His
 20 25
 50

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

60

557

Met Val Phe Ser Val Ser Ser Ala Leu Ala Leu Leu Met Leu Leu
 1 5 10 15

5 Arg Ser Ser Asp Leu Ala Lys Lys Thr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO: 343:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ser Leu Glu Phe Tyr Gln Lys Lys Lys Ser Arg Trp Pro Phe Ser
 1 5 10 15

20 Asp Glu Cys Ile Pro Trp Glu Val Trp Thr Val Lys Val His Val Val
 20 25 30

Ala Leu Ala Thr Glu Gln Glu Arg Gln Ile Cys Arg Glu Lys Val Gly
 35 40 45

25

Glu Lys Leu Cys Glu Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg
 50 55 60

30 His Glu Tyr Leu Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val
 65 70 75 80

Phe Asp Thr Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser
 85 90 95

35 Phe Gln Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Thr Met Arg
 100 105 110

Arg Leu Ile Lys Asp Thr Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly
 115 120 125

40

Ser Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu
 130 135 140

45 Gly Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp Xaa
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 344:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Phe Leu Leu Pro Leu Pro Ala Ala Gly Arg Val Val Val Arg Arg
 1 5 10 15

60 Leu Ala Val Arg Arg Phe Gly Ser Arg Ser Leu Ser Thr Ala Asp Met

	20	25	30
	Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp Asp		
	35	40	45
5	Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu Ala		
	50	55	60
10	Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys Ala		
	65	70	75
	Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser Val		
	85	90	95
15	Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln Glu		
	100	105	110
	Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala Gly		
	115	120	125
20	Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp Pro		
	130	135	140
25	Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu Tyr		
	145	150	155
	Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala Lys		
	165	170	175
30	Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu Phe		
	180	185	190
	Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala Asn		
	195	200	205
35	Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu Lys		
	210	215	220
40	Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp Ile		
	225	230	235
	Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser Asp		
	245	250	255
45	Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn Ala		
	260	265	270
	Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp Ser		
	275	280	285
50	Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg Ala		
	290	295	300
55	Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala Ala		
	305	310	315
	Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys Glu		
	325	330	335
60	Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg Ala		

	340		345		350
	Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly Arg				
	355		360		365
5	Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro Lys				
	370		375		380
10	Xaa Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala Leu				
	385		390		400
	Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp Asn				
		405		410	415
15	Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg Met				
		420		425	430
	Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu Ala				
20		435		440	445
	Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr Ala				
		450		455	460
25	Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His Leu				
		465		470	475
	Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu Arg				
		485		490	495
30	Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu Leu				
		500		505	510
	Arg Phe Ser Gln Asp Asn Ala Xaa				
35		515		520	

(2) INFORMATION FOR SEQ ID NO: 345:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 39 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:
	Thr Ile Leu Phe Leu Phe Leu Gln Leu Ser Ala Leu Arg Leu Ile Val
	1 5 10 15
50	Gly Lys Asp Ser Ile Asp Ile Asp Ile Ser Ser Arg Arg Arg Glu Asp
	20 25 30
	Gln Ser Leu Arg Leu Asn Ala
	35

55

(2) INFORMATION FOR SEQ ID NO: 346:

60	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

5 Met Thr Ser Glu Leu Asp Ile Phe Val Gly Asn Thr Thr Leu Ile Asp
 1 5 10 15
 Glu Asp Val Tyr Arg Leu Trp Leu Asp Gly Tyr Ser Val Thr Asp Ala
 20 25 30
 10 Val Ala Leu Arg Val Arg Ser Gly Ile Leu Glu Gln Thr Gly Ala Thr
 35 40 45
 Ala Ala Val Leu Gln Ser Asp Thr Met Asp His Tyr Arg Thr Phe His
 15 50 55 60
 Met Leu Glu Arg Leu Leu His Ala Pro Pro Lys Leu Leu His Gln Leu
 65 70 75 80
 20 Ile Phe Gln Ile Pro Pro Ser Arg Gln Ala Leu Leu Ile Glu Arg Tyr
 85 90 95
 Tyr Ala Phe Asp Glu Ala Phe Val Arg Glu Val Leu Gly Lys Lys Leu
 100 105 110
 25 Ser Lys Gly Thr Lys Lys Asp Leu Asp Asp Ile Ser Thr Lys Thr Gly
 115 120 125
 Ile Thr Leu Lys Ser Cys Arg Arg Gln Phe Asp Asn Phe Lys Arg Val
 30 130 135 140
 Phe Lys Val Val Glu Glu Met Arg Gly Ser Leu Val Asp Asn Ile Gln
 145 150 155 160
 35 Gln His Phe Leu Leu Ser Asp Arg Leu Ala Arg Asp Tyr Ala Ala Ile
 165 170 175
 Val Phe Phe Ala Asn Asn Arg Phe Glu Thr Gly Lys Lys Lys Leu Gln
 180 185 190
 40 Tyr Leu Ser Phe Gly Asp Phe Ala Phe Cys Ala Glu Leu Met Ile Gln
 195 200 205
 Asn Trp Thr Leu Gly Pro Val Asp Ser Gln Met Asp Asp Met Asp Met
 45 210 215 220
 Asp Leu Asp Arg Asn Phe Ser Arg Thr Xaa
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

60 Met Ala Ala Ala Val Ala Gly Met Leu Arg Gly Gly Leu Leu Pro Gln

561

1 5 10 15
 Ala Gly Arg Leu Pro Thr Leu Gln Thr Val Arg Tyr Gly Ser Lys Ala
 20 25 30
 5 Val Thr Arg His Arg Arg Val Met His Phe Gln Arg Gln Lys Leu Met
 35 40 45
 10 Ala Val Thr Glu Tyr Ile Pro Pro Lys Pro Ala Ile His Pro Ser Cys
 50 55 60
 Leu Pro Ser Pro Pro Ser Pro Pro Gln Glu Glu Ile Gly Leu Ile Arg
 65 70 75 80
 15 Leu Leu Arg Arg Glu Ile Ala Ala Val Phe Gln Asp Asn Arg Met Ile
 85 90 95
 Ala Val Cys Gln Asn Val Ala Leu Ser Ala Glu Asp Lys Leu Leu Ile
 100 105 110
 20 Ala Thr Pro Ala Ala Glu Thr Gln Asp Pro Asp Glu Gly Leu Pro Gln
 115 120 125
 25 Pro Gly Pro Glu Ser Pro Ser Trp Arg Ile Pro Ser Thr Lys Ile Cys
 130 135 140
 Cys Pro Phe Leu Trp Gly Thr Thr Cys Cys Trp Ser Val Lys Ser Pro
 145 150 155 160
 30 Arg Ser Arg Arg Trp Tyr Gly Ser Xaa
 165

35 (2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Lys Arg Ser Phe Leu Leu Pro Leu Leu Val Gly Phe Leu Asp
 1 5 10 15
 45 Thr Ala His Leu Ile Leu Leu Glu Thr Leu Ser Val Cys Leu Trp Leu
 20 25 30
 50 Pro Ser Leu Ile Asp Ser Arg Cys Val Met Ser
 35 40

55 (2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Lys Glu Gly Pro Pro Cys Lys Arg His His Tyr Tyr Gln Asn Cys
 1 5 10 15
 5 Gly Ala Lys Leu Leu Val Ser Leu Phe Gly Glu Thr Asn Gln Ile His
 20 25 30
 Leu Leu Glu Thr Gln Val Gly Thr Glu Lys Gly Gly Glu Arg Ile Trp
 35 40 45
 10 Glu Glu Lys Trp Arg Ile Ser Ser Thr Val Leu Phe Ile Ser Val Asn
 50 55 60
 Ser Tyr Val Glu Gly Ser Val Leu Glu Ile Lys Leu Phe Tyr
 15 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Ser Glu Ile Leu Ser Leu Leu Phe Cys Leu Leu Gly Pro Ala Leu
 1 5 10 15
 30 Asp Glu Arg Arg Glu Glu Lys Asp
 20

35 (2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 45 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 50 55 60
 55 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 60

Arg Pro Ala Gly Gly Ala His Leu Cys Ala Met Xaa Val Ile Glu Gly
 100 105 110
 5 Leu Val Val Asp Val Gly Glu Arg Ile Leu His Gly Gln Arg Glu Val
 115 120 125
 Gly Gln Val Ser Gln Val Leu Pro Ala Leu Ser Leu Gly Leu Val Phe
 130 135 140
 10 Leu Cys Gln Gly Thr Val Glu Lys Val Ser Gly Ala Ala His Cys Ser
 145 150 155 160
 Ser Leu Leu Cys Cys Leu Pro Trp Gln Cys Ser Gly Gly Gly Phe Pro
 165 170 175
 15 Thr Xaa Arg Cys Ser Arg Pro Tyr Phe Ser Ser His Lys Gly Val Ala
 180 185 190
 Ala Thr Leu Ala Leu Thr Cys His Cys Asp Lys Val His Val Ala Gly
 195 200 205
 Leu Gly Lys Asp Trp Ala Ile Glu Gln Arg Arg Arg Thr Cys Glu Ser
 210 215 220
 25 Asp Xaa Glu Xaa Xaa Pro Phe Thr Leu Ala Gly Leu Val Leu Val Leu
 225 230 235 240
 Arg Phe Cys Gln Val Val Leu Val Trp Ile Pro Gln Leu Gly Asp Lys
 245 250 255
 30 His Trp Arg Gly Met Thr Arg Leu Gly Arg Val Ser Leu Thr Ser Ser
 260 265 270
 Ile Xaa
 35

(2) INFORMATION FOR SEQ ID NO: 352:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Ile Phe Thr Ser Val Thr Lys Gly Ile Leu Leu Ile Ala Leu Trp
 1 5 10 15
 50 Val Pro Leu Phe His Phe Met Leu Ile Asp Ser Ile Leu Gly Pro Ser
 20 25 30
 Arg Leu Leu Thr Asp Gly Val Pro Phe Asn Pro Trp His Val Xaa
 35 40 45
 55

(2) INFORMATION FOR SEQ ID NO: 353:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

5

Met Lys Thr

1

10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

20 Met Ser Ile Ser Gly Thr Asp Gly Leu Ile Leu Leu Val Gly Leu
1 5 10 15

Glu Ala Xaa Val Arg Ser Ser Lys Lys Trp Ile Pro Lys Ala Leu Xaa
20 25 30

25 Val Thr Gln Ala Lys Trp Asn Ser Trp Pro Ser Arg Arg Asn Ala Gly
35 40 45

Phe Ala Leu His

50

30

(2) INFORMATION FOR SEQ ID NO: 355:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

40

Met Glu His Cys Leu Tyr His Ser Val His Gly Ile Asn Pro Tyr Ile
1 5 10 15

45 His Lys Asn Thr His Pro Ser Ile Asn Ile Tyr Met Val Trp Asp Glu
20 25 30

Gln Val Asn Ser Phe Glu Arg Glu Phe Val Pro Phe Phe Phe Leu Ile
35 40 45

50 Ile Leu Leu Asn Cys Cys Gln Leu Ser Asn Lys Gln Thr Glu Lys Leu
50 55 60

Phe Gly Lys Thr Leu His Thr Pro Phe Leu Ser Ser Ala Leu Lys Tyr
65 70 75 80

55

Arg Leu Asn Thr His Ile Leu Pro Val Phe Ser Tyr Ser Asp Ser Ile
85 90 95

60 Leu Thr Cys His Leu Ile Leu Ala Ser Tyr Phe Ser His Val Tyr Leu
100 105 110

565

Pro Val Thr Cys Ile Cys Tyr Leu Asn Arg Lys Lys Asn Ile Gln Lys
 115 120 125

5 Lys Lys Asn Xaa
 130

10 (2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly Ser Arg Asp His Leu Phe Lys Val Leu Val Val Gly Asp Ala
 1 5 10 15
 20 Ala Val Gly Lys Thr Ser Leu Val Gln Asp Tyr Ser Gln Asp Ser Phe
 20 25 30
 Ser Lys His Tyr Lys Ser Thr Val Gly Val Asp Phe Ala Leu Lys Val
 25 35 40 45
 Leu Gln Trp Ser Asp Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile
 50 55 60
 30 Ala Gly Gln Glu Arg Phe Thr Ser Met Thr Arg Leu Tyr Tyr Arg Asp
 65 70 75 80
 Ala Ser Ala Cys Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe
 85 90 95
 35 Ser Asn Ser Gln Arg Trp Lys Gln Asp Leu Asp Ser Lys Leu Thr Leu
 100 105 110
 Pro Asn Gly Glu Pro Val Pro Cys Leu Leu Leu Ala Asn Lys Cys Asp
 40 115 120 125
 Leu Ser Pro Trp Ala Val Ser Arg Asp Gln Ile Asp Arg Phe Ser Lys
 130 135 140
 45 Glu Asn Gly Phe Thr Gly Trp Thr Glu Thr Ser Val Lys Glu Asn Lys
 145 150 155 160
 Asn Ile Asn Glu Ala Met Arg Val Leu Ile Glu Lys Met Met Arg Asn
 165 170 175
 50 Ser Thr Glu Asp Ile Met Ser Leu Ser Thr Gln Gly Asp Tyr Ile Asn
 180 185 190
 Leu Gln Thr Lys Ser Ser Ser Trp Ser Cys Cys Xaa
 55 195 200

60 (2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ile Ser Leu Ile Phe Gln Leu Glu Glu Lys Leu Val Glu Lys
 .1 . 5 10 15

10 Phe Phe Phe Phe Leu Phe Phe Phe Leu Lys Lys Gly Ser Gln Gly Ser
 20 25 30

Asn Leu Lys Ile Val Pro Arg His Met Arg Val Val Leu Arg Gly
 35 40 45
 15

(2) INFORMATION FOR SEQ ID NO: 358:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Thr Tyr Val Thr Cys Leu His Val Cys Leu Leu Val Glu Phe Leu
 1 5 10 15

30 Asn Ser Gln Leu Thr Asn His Arg Lys Tyr Tyr Phe Leu Ser Tyr Gly
 20 25 30

Phe Trp Phe Thr Gly Leu Arg Gly Phe Ser Glu Tyr Leu Trp Pro Gln
 35 40 45

35 Gln His Thr Ser Phe His Pro Asn Arg Asn Glu Ile Asn Phe Val Ser
 50 55 60

Thr Asp Asn Arg Ile Trp Val Thr Xaa
 65 70
 40

(2) INFORMATION FOR SEQ ID NO: 359:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys
 1 5 10 15

55 Lys Glu Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
 20 25 30

Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
 35 40 45

60 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe

(2) . INFORMATION FOR SEO ID NO: 360:

15

20

Met Gly Phe Pro Gln Trp His Leu Gly Asn His Ala Val Glu Pro Val
1 5 10 15

25 Thr Ser Ile Leu Leu Leu Phe Leu Leu Met Met Leu Gly Val Arg Gly
20 25 30

Leu Leu Leu Val Gly Leu Val Tyr Leu Val Ser His Leu Ser Gln Arg
35 40 45

30

35

(2) INFORMATION FOR SEO ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 361:

45 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
1 5 10 15

45

Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
20 25 30

50 Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
 35 40 45

Met Pro Asn Val Arg Glu Leu Ala Glu Ser Asp Phe Ala Ser Thr Phe
50 55 60

55

Arg Leu Leu Thr Val Phe Ala Tyr Gly Thr Tyr Ala Asp Tyr Leu Ala
65 70 75 80

[illegible]

Arg His Leu Ser Val Val Thr Leu Ala Ala Lys Val Lys Cys Ile Pro
 100 105 110

5 Tyr Ala Val Leu Leu Glu Ala Leu Ala Leu Arg Asn Val Arg Gln Leu
 115 120 125

Glu Asp Leu Val Ile Glu Ala Val Tyr Ala Asp Val Leu Arg Gly Ser
 130 135 140

10 Leu Asp Gln Arg Asn Gln Arg Leu Glu Val Asp Tyr Ser Ile Gly Arg
 145 150 155 160

Asp Ile Gln Arg Gln Asp Leu Ser Ala Ile Ala Arg Thr Leu Xaa Lys
 15 165 170 175

Asn His Xaa

20

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Met Lys Ser Ser Ser Leu Phe Phe Phe Phe Leu Ala His Phe Ile His
 1 5 10 15

Ser His Asp Leu Pro Gly Leu Cys Arg
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 363:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

45 Met Lys Phe Ala Ala Ser Gly Xaa Phe Leu His His Met Ala Gly Leu
 1 5 10 15

Ser Ser Ser Lys Leu Ser Met Ser Lys Ala Leu Pro Leu Thr Lys Val
 20 25 30

Val Gln Asn Asp Ala Tyr Thr Ala Pro Ala Leu Pro Ser Ser Ile Arg
 35 40 45

55 Thr Lys Ala Leu Thr Asn Met Ser Arg Thr Leu Val Asn Lys Glu Glu
 50 55 60

Pro Pro Lys Glu Leu Pro Ala Ala Glu Pro Val Leu Ser Pro Leu Glu
 65 70 75 80

60

Gly Thr Lys Met Thr Val Asn Asn Leu His Pro Arg Val Thr Glu Glu
 85 90 95
 5 Asp Ile Val Glu Leu Phe Cys Val Cys Gly Ala Leu Lys Arg Ala Arg
 100 105 110
 Leu Val His Pro Gly Val Ala Glu Val Val Phe Val Lys Lys Asp Asp
 115 120 125
 10 Ala Ile Thr Ala Tyr Lys Lys Tyr Asn Asn Arg Cys Leu Asp Gly Gln
 130 135 140
 Pro Met Lys Cys Asn Leu His Met Asn Gly Asn Val Ile Thr Ser Asp
 145 150 155 160
 15 Gln Pro Ile Leu Leu Arg Leu Ser Asp Ser Pro Ser Met Lys Lys Glu
 165 170 175
 Ser Glu Leu Pro Arg Arg Val Asn Ser Ala Ser Ser Ser Asn Pro Pro
 180 185 190
 Ala Glu Val Asp Pro Asp Thr Ile Leu Lys Ala Leu Phe Lys Ser Ser
 195 200 205
 25 Gly Ala Ser Xaa Thr Thr Gln Pro Thr Glu Phe Lys Ile Lys Leu Xaa
 210 215 220

30

(2) INFORMATION FOR SEQ ID NO: 364:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

40

Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala
 1 5 10 15

45

Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn
 20 25 30

Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser
 35 40 45

50

Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile
 50 55 60

Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn
 65 70 75 80

55

Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg
 85 90 95

60

Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro
 100 105 110

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys
 115 120 125

5 Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys
 130 135 140

Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser
 145 150 155 160

10 Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys Thr
 165 170 175

Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn Glu Thr
 180 185 190

15 Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp Leu Pro Ser
 195 200 205

20 Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu Val Pro Ser Ser
 210 215 220

Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln His Ala Glu Glu Gln
 225 230 235 240

25 Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys Glu Phe Lys Asp Leu His
 245 250 255

Cys Ser Lys Asp Ser Thr Leu Ala Glu Glu Glu Ser Glu Phe Pro Ser
 260 265 270

30 Thr Ser Ile Ser Ala Val Leu Ser Asp Leu Ala Asp Leu Arg Ser Cys
 275 280 285

35 Asp Gly Gln Ala Leu Pro Ser Gln Asp Pro Glu Val Ala Leu Ser Leu
 290 295 300

Ser Cys Gly His Ser Arg Gly Leu Phe Ser His Met Gln Gln His Asp
 305 310 315 320

40 Ile Leu Asp Thr Leu Cys Arg Thr Ile Glu Ser Thr Ile His Val Val
 325 330 335

Thr Arg Ile Ser Gly Lys Gly Asn Gln Ala Ala Ser Xaa
 340 345

45

(2) INFORMATION FOR SEQ ID NO: 365:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Leu His Gln Asp His Ile Thr Phe Ala Met Leu Leu Ala Arg Ile
 1 5 10 15

60

Lys Leu Lys Gly Thr Val Gly Glu Pro Thr Tyr Asp Ala Glu Phe Gln

	20	25	30
	His Phe Leu Arg Gly Asn Glu Ile Val Leu Ser Ala Gly Ser Thr Pro		
	35	40	45
5	Arg Ile Gln Gly Leu Thr Val Glu Gln Ala Glu Ala Val Val Arg Leu		
	50	55	60
	Ser Cys Leu Pro Ala Phe Lys Asp Leu Ile Ala Lys Val Gln Ala Asp		
10	65	70	75 80
	Glu Gln Phe Gly Ile Trp Leu Asp Ser Ser Ser Pro Glu Gln Thr Val		
	85	90	95
15	Pro Tyr Leu Trp Ser Glu Glu Thr Pro Ala Thr Pro Ile Gly Gln Ala		
	100	105	110
	Ile His Arg Leu Leu Leu Ile Gln Ala Phe Arg Pro Asp Arg Leu Leu		
	115	120	125
20	Ala Met Ala His Met Phe Val Ser Thr Asn Leu Gly Glu Ser Phe Met		
	130	135	140
	Ser Ile Met Glu Gln Pro Leu Asp Leu Thr His Ile Val Xaa Thr Glu		
25	145	150	155 160
	Val Lys Pro Asn Thr Pro Val Leu Met Cys Ser Val Pro Gly Tyr Asp		
	165	170	175
30	Ala Ser Gly His Val Glu Asp Leu Ala Ala Glu Gln Asn Thr Gln Ile		
	180	185	190
	Thr Ser Ile Ala Ile Gly Ser Ala Glu Gly Phe Asn Gln Ala Asp Lys		
	195	200	205
35	Ala Ile Asn Thr Ala Val Lys Ser Gly Arg Trp Val Met Leu Lys Asn		
	210	215	220
	Val His Leu Ala Pro Gly Trp Leu Met Gln Leu Glu Lys Lys Leu His		
40	225	230	235 240
	Ser Leu Gln Pro His Ala Cys Phe Arg Leu Phe Leu Thr Met Glu Ile		
	245	250	255
45	Asn Pro Lys Val Pro Val Asn Leu Leu Arg Ala Gly Arg Ile Phe Val		
	260	265	270
	Phe Glu Pro Pro Pro Gly Xaa Lys Ala Asn Met Leu Arg Thr Phe Ser		
	275	280	285
50	Ser Ile Pro Val Ser Arg Ile Cys Lys Ser Pro Asn Glu Arg Ala Arg		
	290	295	300
	Leu Tyr Phe Leu Leu Ala Trp Phe His Ala Ile Ile Gln Glu Arg Leu		
55	305	310	315 320
	Arg Tyr Ala Pro Leu Gly Trp Ser Lys Lys Tyr Glu Phe Gly Glu Ser		
	325	330	335
60	Asp Leu Arg Ser Xaa Cys Asp Thr Val Asp Thr Trp Leu Asp Asp Thr		

	340		345		350
Ala Lys Gly Arg Gln Asn Ile Ser Pro Asp Lys Ile Pro Trp Ser Ala 355 360 365					
Leu Lys Thr Leu Met Ala Gln Ser Ile Tyr Gly Gly Arg Val Asp Asn 370 375 380					
Glu Phe Asp Gln Arg Leu Leu Asn Thr Phe Leu Glu Arg Leu Phe Thr 385 390 395 400					
Thr Arg Ser Phe Asp Ser Glu Phe Lys Leu Ala Cys Lys Val Asp Gly 405 410 415					
His Lys Asp Ile Gln Met Pro Asp Gly Met Gln Ala Arg Gly Val Cys 420 425 430					
Ala Val Gly Gly Val Ala Pro Arg His Pro Asp Ala Leu Leu Ala Gly 435 440 445					
Pro Ala Gln Gln Arg Arg Glu Ser Pro Pro Tyr His Thr Gly Cys Gly 450 455 460					
His Asp Gln 465					

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

[illegible]

Cys Ala Gln Ile Trp Thr Ser Ser Ser His Gly Ser Gly Ala Gly Ser
 130 135 140

5 Met Xaa Gly Ser Gly Asn Pro Xaa
 145 150

10 (2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr
 1 5 10 15

20 Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly
 20 25 30

Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu
 35 40 45

25 Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile
 50 55 60

30 Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro
 65 70 75 80

Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val
 85 90 95

35 Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile
 100 105 110

Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met
 115 120 125

40 Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln
 130 135 140

45 Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp
 145 150 155 160

Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Xaa Leu
 165 170 175

50 Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln
 180 185 190

Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile
 195 200 205

55 Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys
 210 215 220

60 Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn
 225 230 235 240

574

Leu Ile Glu Arg Gln Lys Lys Val Lys Leu Phe Cys Leu Glu Thr Phe
 245 250 255
 5 Leu Ser Asp Leu Ile Ala His Gln Lys Gly Gln Ile Glu Lys Gln Pro
 260 265 270
 Pro Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu Trp Pro Asp Gly Lys
 275 280 285
 10 Pro Leu Glu Arg Lys Leu Ile Leu Val Gln Val Ile Pro Val Val Ala
 290 295 300
 Arg Met Ile Tyr Glu Met Phe Ser Gly Asp Phe Thr Arg Ser Phe Asp
 15 305 310 315 320
 Ser Gly Ser Val Arg Leu Gln Ile Ser Thr Pro Asp Ile Lys Asp Asn
 325 330 335
 20 Ile Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile Leu Gln Thr Gln Glu
 340 345 350
 Ser Trp Gln Pro Met Gln Pro Thr Pro Ser Met Gln Leu Pro Pro Ala
 355 360 365
 25 Leu Pro Pro Gln Xaa
 370

30

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

40 Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
 1 5 10 15
 Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
 20 25 30
 45 Trp Gly Phe Gly Arg Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
 35 40 45
 Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
 50 55 60
 50 His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
 65 70 75 80
 Pro Asn Xaa
 55

60

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15

10 Tyr Trp Thr Met Xaa
 20

15 (2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15

25 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30

30 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45

Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60

35 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80

Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95

40 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110

45 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125

Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140

50 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160

Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175

55 Glu Asp Gln Thr Lys Pro Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val
 180 185 190

60 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205

576

Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220

5 Val Thr Pro
 225

10 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Phe Leu Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln
 1 5 10 15

20

Leu Lys Ile Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu
 20 25 30

25

Lys Ile Ile Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser
 35 40 45

Trp Ala Ile Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn
 50 55 60

30

Lys Thr Ala Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr Xaa
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ala Val Phe Pro Cys Cys Pro Phe Leu Thr Leu Met Leu Pro
 1 5 10 15

45

Leu Leu Glu Cys Leu Val Gly Met Ile Met Cys Tyr Leu Gly Ile Ser
 20 25 30

50

Phe Thr Asp Thr Arg Lys Thr Ala Gly Leu Lys Lys Lys Lys Lys Lys
 35 40 45

Lys Xaa Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

60

577

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

5 Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
1 5 10 15
Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Ala Ser Tyr Leu Trp
20 25 30
10 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Ser Trp Ala Cys
35 40 45
15 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu Xaa
50 55 60

(2) INFORMATION FOR SEQ ID NO: 374:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
1 5 10 15
30 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
20 25 30
Ile Leu Phe Phe Ile Val Phe Xaa
35 40
35

(2) INFORMATION FOR SEQ ID NO: 375:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Cys Ser Gly Gln Ser Gln Val Trp Lys Met Ala Leu Gln Ala Leu
1 5 10 15
50 Asp Ser Glu Thr Val Val Ile Leu Pro Asp Met His Leu Ile Leu Ser
20 25 30
Leu Arg Leu Ile His Asn Ala Arg Pro Cys Leu Xaa
35 40
55

(2) INFORMATION FOR SEQ ID NO: 376:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

578

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

5 Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp
 1 5 10 15
 Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg
 20 25 30
 10 Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val
 35 40 45
 Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp
 15 50 55 60
 Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser
 65 70 75 80
 20 Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg
 85 90 95
 Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu
 100 105 110
 25 Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys
 115 120 125
 Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu
 30 130 135 140
 Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr
 145 150 155 160
 35 Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met
 165 170 175
 Ile His Thr Gly Glu Lys His Tyr Asn Val Arg Ser Val Asp Leu Leu
 180 185 190
 40 Val Asp Lys Arg His Leu Leu Ile Gly Thr Xaa
 195 200

45

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

50 Met Leu Pro Arg Arg Thr Phe Tyr Phe Tyr Phe Ile Phe Ile Phe Phe
 1 5 10 15
 Leu Ala Ser Phe Trp Gly Phe Thr Leu Arg Ala Ser Phe
 20 25

60

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

5
 10 Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu Met
 1 5 10 15
 Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val Leu
 20 25 30
 15 Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu Trp
 35 40 45
 Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg Met
 20 50 55 60
 Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val Gln
 65 70 75 80
 25 Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu Asn
 85 90 95
 Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met Pro Ser Phe
 100 105 110
 30 Phe Ser Cys His Leu Phe Cys Thr Leu Arg Trp Lys Tyr Phe Glu Val
 115 120 125
 Phe Tyr Asn His Lys Phe Leu Xaa
 35 130 135

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

40
 45
 50 Met Ala Trp Arg Arg Arg Glu Pro Ala Ser Gly Leu Ala Ala Cys Trp
 1 5 10 15
 Leu Trp Arg Cys Ser Pro Trp Pro Cys Ala Cys Pro Gly Pro Gly Ala
 20 25 30
 Gly Leu Ser Ser Gly Ser Arg Pro Trp
 55 35 40

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

580

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

5 Met Glu Phe Leu Lys Val Ala Arg Arg Asn Lys Arg Glu Gln Leu Glu
 1 5 10 15
 10 Gln Ile Gln Lys Glu Leu Ser Val Leu Glu Glu Asp Ile Lys Arg Val
 20 20 25 30
 Glu Glu Met Ser Gly Leu Tyr Ser Pro Val Ser Glu Asp Ser Thr Val
 35 40 45
 15 Pro Gln Phe Glu Ala Pro Ser Pro Ser His Ser Ser Ile Ile Asp Ser
 50 55 60
 Thr Glu Tyr Ser Gln Pro Pro Gly Phe Ser Gly Ser Ser Gln Thr Lys
 65 70 75 80
 20 Lys Gln Pro Trp Tyr Asn Ser Thr Leu Ala Ser Arg Arg Lys Arg Leu
 85 90 95
 25 Thr Ala His Phe Glu Asp Leu Glu Gln Cys Tyr Phe Ser Thr Arg Met
 100 105 110
 Ser Arg Ile Ser Asp Asp Ser Arg Thr Ala Ser Gln Leu Asp Glu Phe
 115 120 125
 30 Gln Glu Cys Leu Ser Lys Phe Thr Arg Tyr Asn Ser Val Arg Pro Leu
 130 135 140
 Ala Thr Leu Ser Tyr Ala Ser Asp Leu Tyr Asn Gly Ser Ser Ile Val
 145 150 155 160
 35 Ser Ser Ile Glu Phe Asp Arg Asp Cys Asp Tyr Phe Ala Ile Ala Gly
 165 170 175
 40 Val Thr Lys Lys Ile Lys Val Tyr Glu Tyr Asp Thr Val Ile Gln Asp
 180 185 190
 Ala Val Asp Ile His Tyr Pro Glu Asn Glu Met Thr Cys Asn Ser Lys
 195 200 205
 45 Ile Ser Cys Ile Ser Trp Ser Ser Tyr His Lys Asn Leu Leu Ala Ser
 210 215 220
 Ser Asp Tyr Glu Gly Thr Val Ile Leu Trp Asp Gly Phe Thr Gly Gln
 225 230 235 240
 50 Arg Ser Lys Val Tyr Gln Glu His Glu Lys Arg Cys Trp Ser Val Asp
 245 250 255
 Phe Asn Leu Met Asp Pro Lys Leu Leu Ala Ser Gly Ser Asp Asp Ala
 260 265 270
 Lys Val Lys Leu Trp Ser Thr Asn Leu Asp Asn Ser Val Ala Ser Ile
 275 280 285
 60 Glu Ala Lys Ala Asn Val Cys Cys Val Lys Phe Ser Pro Ser Ser Arg

581

290 295 300

Tyr His Leu Ala Phe Gly Cys Ala Asp His Cys Val His Tyr Tyr Asp
305 310 315 320

5 Leu Arg Asn Thr Lys Gln Pro Ile Met Val Phe Lys Gly His Arg Lys
325 330 335

10 Ala Val Ser Tyr Ala Lys Phe Val Ser Gly Glu Glu Ile Val Ser Ala
340 345 350

Ser Thr Asp Ser Gln Leu Lys Leu Trp Asn Val Gly Lys Pro Tyr Cys
355 360 365

15 Leu Arg Ser Phe Lys Gly His Ile Asn Glu Lys Asn Phe Val Gly Leu
370 375 380

20 Ala Ser Asn Gly Asp Tyr Ile Ala Cys Gly Ser Glu Asn Asn Ser Leu
385 390 395 400

Tyr Leu Tyr Tyr Lys Gly Leu Ser Lys Thr Leu Leu Thr Phe Lys Phe
405 410 415

25 Asp Thr Val Lys Ser Val Leu Asp Lys Asp Arg Lys Glu Asp Asp Thr
420 425 430

Asn Glu Phe Val Ser Ala Val Cys Trp Arg Ala Leu Pro Asp Gly Glu
435 440 445

30 Ser Asn Val Leu Ile Ala Ala Asn Ser Gln Gly Thr Ile Lys Val Leu
450 455 460

Glu Leu Val Xaa
465

35

(2) INFORMATION FOR SEQ ID NO: 381:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

45 Met Arg Lys Glu Asp Gly Phe Trp Phe Phe Phe Leu Phe Phe Phe
1 5 10 15

50 Val Val Gly Ser Lys Phe Val Asn Gly Asn Lys Leu Val
20 25

(2) INFORMATION FOR SEQ ID NO: 382:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Pro Leu Ala Pro Tyr Cys Asp Leu Leu Val Ala Leu Ser Phe Ala
 1 5 10 15
 5 Leu Val Leu Glu Ser Pro Val Asp Ser Ser Asp Phe Thr
 20 25

10 (2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Asn Ser Leu Val Ser Trp Gln Leu Leu Leu Phe Leu Cys Ala Thr
 1 5 10 15
 20 His Phe Gly Glu Pro Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg
 20 25 30
 25 Pro Thr Gly Gln Gln Leu Glu Ser Leu Gly Leu Leu Ala Pro Gly Glu
 35 40 45
 Gln Ser Leu Pro Cys Thr Glu Arg Lys Pro Ala Ala Thr Ala Arg Leu
 50 55 60
 30 Ser Arg Arg Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser
 65 70 75 80
 Pro Gln Gln Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala
 85 90 95
 35 Pro Gln Gly Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr
 100 105 110
 40 Asn Trp Asn Ser Phe Gly Leu Arg Phe Gly Lys Arg Glu Ala Ala Pro
 115 120 125
 Gly Asn His Gly Arg Ser Ala Gly Arg Gly
 130 135

45

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Ser Cys Phe Ile Asp Ser Xaa Asp Ser Lys Ile Leu His Leu Leu
 1 5 10 15
 Val Val Ser Phe Ile Cys Xaa Leu Phe Leu Leu Ile Leu Thr His Gly
 20 25 30
 60

Ile Leu Ile Leu Arg Xaa Phe Phe Ser Val Xaa Xaa His Ser Leu Lys
 35 40 45
 Asn Asn Leu Glu Glu Tyr Leu Ile Leu Met Asn Lys Ala Leu Leu Thr
 5 50 55 60
 Arg Glu Asp Phe Phe Val Leu Pro Xaa Ala
 65 70
 10
 (2) INFORMATION FOR SEQ ID NO: 385:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 521 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:
 20 Met Ser Ala Gly Glu Val Glu Arg Leu Val Ser Glu Leu Ser Gly Gly
 1 5 10 15
 Thr Gly Gly Asp Glu Glu Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu
 20 25 30
 25 Val Glu Arg Pro Glu Glu Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly
 35 40 45
 30 Ile Glu Asp Glu Thr Ala Glu Asn Gly Val Pro Lys Pro Lys Val Thr
 50 55 60
 Glu Thr Glu Asp Asp Ser Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp
 65 70 75 80
 35 Val His Val Thr Ile Gly Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly
 85 90 95
 Ser Tyr Gly Thr Ala Pro Val Asn Leu Asn Ile Lys Thr Gly Gly Arg
 100 105 110
 40 Val Tyr Gly Thr Thr Gly Thr Lys Val Lys Gly Val Asp Leu Asp Ala
 115 120 125
 Pro Gly Ser Ile Asn Gly Val Pro Leu Leu Glu Val Asp Leu Asp Ser
 45 130 135 140
 Phe Glu Asp Lys Pro Trp Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr
 145 150 155 160
 50 Phe Asn Tyr Gly Phe Asn Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys
 165 170 175
 Gln Lys Arg Ile Arg Met Gly Leu Glu Val Ile Pro Val Thr Ser Thr
 180 185 190
 55 Thr Asn Lys Ile Thr Val Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys
 195 200 205
 Glu Thr Ala Leu Pro Ser Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser
 60 210 215 220

584

Leu Phe Lys Thr Gly Leu Pro Pro Ser Arg Arg Leu Pro Gly Ala Ile
 225 230 235 240
 5 Asp Val Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg
 245 250 255
 Arg Ala Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala
 260 265 270
 10 Thr Glu Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro
 275 280 285
 Gly Ala Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro
 290 295 300
 15 Pro Thr Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Phe Pro
 305 310 315 320
 20 Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu Ile Pro Thr Ile Glu Ser
 325 330 335
 Gly His Ser Ser Gly Tyr Asp Ser Arg Ser Ala Arg Ala Phe Pro Tyr
 340 345 350
 25 Gly Asn Val Ala Phe Pro His Leu Pro Gly Ser Ala Pro Ser Trp Pro
 355 360 365
 30 Ser Leu Val Asp Thr Ser Lys Gln Trp Asp Tyr Tyr Ala Arg Arg Glu
 370 375 380
 Lys Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 385 390 395 400
 35 Arg Asp Arg Glu Arg Glu Arg Thr Arg Glu Arg Glu Arg Glu Arg Asp
 405 410 415
 His Ser Pro Thr Pro Ser Val Phe Asn Ser Asp Glu Glu Arg Tyr Arg
 420 425 430
 40 Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu Arg His Arg Ala Ser Arg
 435 440 445
 Glu Lys Glu Glu Arg His Arg Glu Arg Arg His Arg Glu Lys Glu Glu
 450 455 460
 45 Thr Arg His Lys Ser Ser Arg Ser Asn Ser Arg Arg Arg His Glu Ser
 465 470 475 480
 50 Glu Glu Gly Asp Ser His Arg Arg His Lys His Lys Lys Ser Lys Arg
 485 490 495
 Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu Pro Ala Pro Glu Gln Glu
 500 505 510
 55 Ser Thr Glu Ala Thr Pro Ala Glu Xaa
 515 520
 60

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

5 Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu
 10 1 5 10 15
 Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val
 20 25 30
 15 Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu
 35 40 45
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 50 55 60
 20 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
 65 70 75 80
 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
 25 85 90 95
 Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
 100 105 110
 30 Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly
 115 120 125
 Val Arg Val Phe Gly Ile Asn Lys Tyr
 130 135
 35

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

40 Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 5 10 15
 Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 50 20 25 30
 Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45
 55 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60
 Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80
 60

586

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
85 90 95

5 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr Leu
100 105 110

Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser Pro
115 120 125

10 Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe Trp
130 135 140

Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr Leu
145 150 155 160

15 Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val Asp
165 170 175

20 Gly Glu Glu Leu Gln Met Glu Pro Val Xaa
180 185

25 (2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met
1

35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

45 Met Leu Ser Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly
1 5 10 15

Tyr Ile Ala Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp
20 25 30

50 Ala Leu Arg Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu
35 40 45

Phe Leu Val Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser
55 60

Asp Leu Pro Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala
65 70 75 80

60 Leu Ala Arg Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala

587

	85	90	95
	Val Ala Phe	Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu	
	100	105	110
5	Leu Arg Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly		
	115	120	125
10	Asp Ser Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys		
	130	135	140
	Leu Thr Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg		
	145	150	155 160
15	Leu Arg His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly		
	165	170	175
	Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg		
	180	185	190
20	Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu		
	195	200	205
25	Leu Ser Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val		
	210	215	220
	Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser		
	225	230	235 240
30	His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser		
	245	250	255
	Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg		
	260	265	270
35	Ala Leu Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly		
	275	280	285
40	Gly Ala Leu Pro Gly His Arg His Leu His Xaa		
	290	295	

(2) INFORMATION FOR SEQ ID NO: 390:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

	Met Gly Pro Gln Gly Trp Val Arg Pro Leu Lys Thr Ala Pro Lys Leu	
	1	5 10 15
55	Gly Glu Ala Ile Arg Leu Ile Leu Phe Leu Asn Phe Val Lys Gln Cys	
	20	25 30
	Ile Ala Ser Val Asn Leu Cys Ile Leu Arg Leu Asn Ile Thr Pro Leu	
	35	40 45

60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

15 Met Tyr Val Asn Tyr Gly Thr Arg Asn Tyr Ser Thr Glu Gly Pro Ala
 1 5 10 15
 Ala Leu Leu Asp Gln Ala Lys Leu Ser Leu Leu Val Trp Val Leu Cys
 20 25 30
 20 Phe Val Leu Leu Phe Val Cys Phe Cys Gly Leu Ser Tyr Val Val Ile
 35 40 45
 Ala Gln Val Pro Val Gly Leu Leu Cys Ile Thr Glu Xaa
 50 55 60
 25

(2) INFORMATION FOR SEQ ID NO: 392:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

35

35 Met Leu Trp Phe Ala Asn Phe Phe Thr Tyr Leu Phe Leu Ser Gln Ser
 1 5 10 15
 40 Val Ala Phe Val His Ile Ser His Ile Gly Val Arg Gln Val Asn Thr
 20 25 30
 Asn Cys Tyr Phe Ser Arg Lys Ser Tyr Cys Tyr Gly Ile Leu Asn Pro
 35 40 45
 45 Ile Asn Cys Ile Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys
 50 55 60
 Lys Lys Lys Lys Ile Pro Ala Gly Arg Xaa Leu Phe Pro Phe Gly
 65 70 75
 50

(2) INFORMATION FOR SEQ ID NO: 393:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

60

Met Pro Gly Ala Phe Ser Glu Thr Val Ile Asn Asp Leu Leu Ser Leu
 1 5 10 15
 5 Phe Leu Val Leu Pro Ala Glu Leu Ser Tyr Ser Thr Leu Ser Gly Val
 20 25 30
 Tyr Arg Asn Ala
 35

10

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

20 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
 1 5 10 15
 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
 20 25 30
 25 Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
 35 40 45
 30 Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
 50 55 60
 Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
 65 70 75 80
 35 Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
 85 90 95
 Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
 100 105 110
 40 Leu Asp Arg Arg Ser Glu Ser Cys Ser Met Leu Pro Trp Xaa Ala Gln
 115 120 125
 Leu Leu Asp Arg Thr Ile Gly Pro Leu Tyr Leu Leu Phe Val Gln Phe
 130 135 140
 45 Ser Pro Ala Phe Ser Arg Thr Ser Pro Trp Arg Ser Pro Lys Asn Phe
 145 150 155 160
 50 Arg Arg Leu Tyr Pro Pro Cys Thr Thr Ser Gly Cys Ala Ala Arg Trp
 165 170 175
 Xaa Phe Ser Xaa
 180

55

(2) INFORMATION FOR SEQ ID NO: 395:

60 (i) SEQUENCE CHARACTERISTICS:

590

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

5

Met Pro Thr Pro Cys Thr Ser Leu Pro Ser Cys Cys Gln His Arg Ser
 1 5 10 15

10

Ile Thr Met Thr Leu
 20

(2) INFORMATION FOR SEQ ID NO: 396:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Leu Ser Leu Leu His Cys
 1 5 10 15

25

Gln Ser Lys His Pro Ile Gln Met Ser Leu Cys Met Cys Val Asn Ile
 20 25 30

30

Ser Leu Val Trp Ser Pro Val Arg Trp Ile Phe Gly Ser Lys Gly Leu
 35 40 45

Phe Ser Val His Leu Gln Ser Ser Gln Arg Pro Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

45

Met Ala Gly Pro Arg Pro Xaa Trp Arg Asp Gln Leu Leu Phe Met Ser
 1 5 10 15

Ile Ile Val Leu Val Ile Val Val Ile Cys Leu Met Leu Tyr Ala Leu
 20 25 30

50

Leu Trp Glu Ala Gly Asn Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly
 35 40 45

Phe Tyr Asn Phe Cys Leu Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys
 50 55 60

55

His Gln Phe Pro Glu Leu Glu Ala Leu Gly Val Pro Arg Val Gly Leu
 65 70 75 80

60

Gly Leu Ala Arg Leu Gly Val Tyr Gly Ser Leu Val Leu Thr Leu Phe
 85 90 95

Ala Pro Gln Pro Leu Leu Leu Ala Gln Cys Asn Xaa Asp Glu Arg Ala
100 105 110

5 Trp Arg Leu Ala Val Gly Phe Leu Ala Val Ser Ser Val Leu Leu Ala
115 120 125

Gly Gly Leu Gly Leu Phe Leu Ser Tyr Val Trp Asn Gly Ser Xaa Ser
130 135 140

10 Pro Ser Arg Gly Leu Gly Phe Xaa
145 150

15 (2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

25 Met Ser Asp Gly Phe Asp Arg Ala Pro Gly Ala Gly Arg Gly Arg Xaa
1 5 10 15

Arg Gly Leu Gly Arg Gly Gly Gly Gly Pro Xaa Gly Gly Gly Phe Pro
20 25 30

30 Xaa Gly Xaa Xaa Pro Ala Glu Arg Xaa Arg His Gln Pro Pro Gln Pro
35 40 45

Lys Ala Pro Gly Phe Leu Gln Pro Xaa Pro Leu Arg Gln Pro Arg Thr
50 55 60

35 Thr Pro Pro Pro Gly Ala Gln Cys Glu Val Pro Ala Ser Pro Gln Arg
65 70 75 80

40 Pro Ser Arg Pro Gly Ala Leu Pro Glu Gln Thr Arg Pro Leu Arg Ala
85 90 95

Pro Pro Ser Ser Gln Asp Lys Ile Pro Gln Gln Asn Ser Glu Ser Ala
100 105 110

45 Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
115 120 125

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
130 135 140

50 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
145 150 155 160

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
165 170 175

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
180 185 190

60 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

592

	195	200	205
	Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr		
	210	215	220
5	Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln		
	225	230	235 240
10	Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala		
	245	250	255
	Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu		
	260	265	270
15	Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly		
	275	280	285
	Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu		
	290	295	300
20	Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val		
	305	310	315 320
	Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu		
	325	330	335
25	Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val		
	340	345	350
30	Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys		
	355	360	365
	Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser		
	370	375	380
35	Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn		
	385	390	395 400
	Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp		
	405	410	415
40	Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe		
	420	425	430
45	Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp		
	435	440	445
	Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu		
	450	455	460
50	Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln Xaa		
	465	470	475 480
55			

(2) INFORMATION FOR SEQ ID NO: 399:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Glu Pro Lys Thr Ile Thr Asp Ala Leu Ala Ser Ser Ile Ile Lys
 1 5 10 15
 10 Ser Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp
 20 25 30
 Ala Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val
 35 40 45
 15 Leu Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly
 50 55 60
 20 Leu Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His
 65 70 75 80
 Ser Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln
 85 90 95
 25 Gln Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val
 100 105 110
 Val Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly
 115 120 125
 30 Gly Pro Val Gly Phe Gln Xaa Tyr Arg Arg Pro Leu Asn Phe Pro Leu
 130 135 140
 35 Arg Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala
 145 150 155 160
 Ser Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met
 165 170 175
 40 Ser Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala
 180 185 190
 Cys Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met
 195 200 205
 45 Val Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys
 210 215 220
 50 Glu Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu
 225 230 235 240
 Ala Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile
 245 250 255
 55 Val Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro
 260 265 270
 60 Trp Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala
 275 280 285

594

Ile Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln
 290 295 300

5 Val Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg
 305 310 315 320

Lys Leu Ala Ala Pro Val Ile Ser Val Leu Leu Ser Leu Cys Val
 325 330 335

10 Pro Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala
 340 345 350

Glu Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met
 355 360 365

15 Val Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys
 370 375 380

Arg Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Val Gly Gln Arg
 385 390 395 400

Leu Val Asn Tyr Glu Arg Lys Ser Gly Lys Gln Gly Ser Ser Pro Pro
 405 410 415

25 Pro Pro Gln Ser Ser Gln Glu
 420

30 (2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15

40 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30

Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45

Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
 50 55 60

50 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu Xaa
 65 70 75

55 (2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

5 Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
 1 5 10 15
 His Cys Trp Gly Leu Pro Leu His Val Ala Pro Leu Cys Arg Gly His
 20 25 30
 10 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala Trp
 35 40 45
 Asn Arg Asn Leu Ala Asn Gln Arg His Phe Phe Cys Pro Ser Ile Phe
 50 55 60
 15 His Thr Cys Pro Thr Val Leu Phe Phe Xaa
 65 70

20 (2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

30 Ala Arg Thr Ile Leu Val Leu Tyr Leu Ser Leu Gln Arg Leu Glu Asn
 1 5 10 15
 Leu Ala Tyr His
 20

35 (2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

45 Met Pro Leu Pro Ser Val Pro Ile Leu Gly Ile Phe Ser Phe Leu Ile
 1 5 10 15
 Pro Ser Ser Gln Gly Val Ser Tyr Thr Lys Leu Pro Ile Ser Ser Pro
 20 25 30
 50 Gln Tyr Ser Pro Phe Val Asn Asp His Phe Ser Phe Leu Asn Pro Phe
 35 40 45
 Pro Val Gln Ile His Thr Gly Phe Ala Arg Val Gly Ser Tyr Met Gln
 50 55 60
 55 Met Pro Leu Val His Leu Cys Leu Leu Gln Thr Ser Leu Met Lys Asn
 65 70 75 80
 60 Ser Gly Val Gln Gln Gly Ser
 85

(2) INFORMATION FOR SEQ ID NO: 404:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile Ile
 1 5 10 15

15 Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala Val
 20 25 30

Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile Thr
 35 40 45

20

Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val Tyr
 50 55 60

25 Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg Asp
 65 70 75 80

Gln Thr Lys Ser Ile Val Glu Lys Ile Pro Ser Lys
 85 90

30

(2) INFORMATION FOR SEQ ID NO: 405:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40 Met Ala Cys Ser Cys Leu Met Ile Gln Ser Phe Ser Thr Ser Ala Leu
 1 5 10 15

Val Leu Phe Tyr Gly
 20

45

(2) INFORMATION FOR SEQ ID NO: 406:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

55

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 1 5 10 15

60 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 20 25 30

Ser Gly Phe Pro Ala Phe Pro Lys Pro Ser Pro Thr Tyr Leu Arg Thr
 35 40 45
 5 Ser Ala Glu Gln Thr Leu Pro Leu Leu Leu Pro His Leu His Gly Leu
 50 55 60
 Cys Leu His Gln Pro Leu His Leu Gly Phe Thr Ala Cys Leu Gly Ser
 65 70 75 80
 10 Ala His Ile Leu Gly Gly Gln Pro Ala Leu Pro Ala Val Pro Glu Pro
 85 90 95
 Tyr Ala Gly His Cys Gln Arg Pro Leu Ala Gly Thr Pro His His Ser
 100 105 110
 15 Cys His Val Gly Pro Ala Asn Arg Gly Arg Arg Ser Glu Ala Trp Val
 115 120 125
 20 Gly Arg Tyr Gln Ala Ala Asn Arg Phe Pro Ile Leu Asn Ala Xaa Cys
 130 135 140
 Glu Arg Arg Thr Pro Ser Thr Val Leu Ser Ala Arg Ile Ser Ser Ala
 145 150 155 160
 25 Thr Met Gly Cys Pro Leu Phe Ala Ile Trp Ala Ala Ser Xaa
 165 170

30

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

35

40 Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15
 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30
 45 Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45
 Thr Glu Gly Ile Pro Cys Gln Arg Tyr Gln Asn Gly Leu His Ile Xaa
 50 55 60

50

55

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

5 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 10 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 15 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 25 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140
 30 His Ser Val Leu Pro Trp Ser Trp Trp Gly Val Lys Ile Ala Pro
 145 150 155 160
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
 165 170 175
 35 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
 180 185 190
 40 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220
 45 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255
 50 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270
 55 Ile Ala Lys Val Lys Ala Asn Xaa
 275 280

60 (2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Xaa Leu Trp Pro Gln Thr Cys Ser Gly Lys Phe Asp Gly Thr Leu
 1 5 10 15
 10 Ala Phe Ser Ile His Xaa Leu Ala Val Ile Leu Gly Asp Gln Leu Thr
 20 25 30
 15 Ala Ala Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp
 35 40 45
 Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu
 50 55 60
 20 Leu His Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe
 65 70 75 80
 Leu Val Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala
 85 90 95
 25 Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr
 100 105 110
 30 Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser
 115 120 125
 Ser Val Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys
 130 135 140
 35 Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu
 145 150 155 160
 Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala
 165 170 175
 40 Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met
 180 185 190
 45 Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn
 195 200 205
 Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln
 210 215 220
 50 Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln
 225 230 235 240
 Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser
 245 250 255
 55 Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser
 260 265 270
 60 Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr Xaa
 275 280

5 (2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu Phe Leu Phe Phe Val Ile Ile Phe Leu Phe Val Phe Leu Ile
 1 5 10 15
 Leu Ile Ile Gln Phe Ser Lys Pro Leu Thr Asn Pro His Pro Pro Ala
 20 25 30
 Gly Xaa Ser Asp Arg Arg Arg Arg Tyr Ser Ser Tyr Arg Ser His Asp
 35 40 45
 His Tyr Gln Arg Gln Arg Val Leu Gln Lys Glu Arg Ala Ile Glu Glu
 50 55 60
 Arg Arg Val Val Phe Ile Gly Lys Ile Pro Gly Arg Met Thr Arg Ser
 65 70 75 80
 Glu Leu Lys Gln Arg Phe Ser Val Phe Gly Glu Ile Glu Glu Cys Thr
 85 90 95
 Ile His Phe Arg Val Gln Gly Asp Asn Tyr Gly Phe Val Thr Tyr Arg
 100 105 110
 Tyr Ala Glu Glu Ala Phe Ala Ala Ile Glu Ser Gly His Lys Leu Arg
 115 120 125
 Gln Ala Asp Glu Gln Pro Phe Asp Leu Cys Phe Gly Gly Arg Arg Xaa
 130 135 140
 Xaa Cys Lys Arg Ser Tyr Ser Asp Leu Asp Ser Asn Arg Glu Asp Phe
 145 150 155 160
 Asp Pro Ala Pro Val Lys Ser Lys Phe Asp Ser Leu Asp Phe Asp Thr
 165 170 175
 Leu Leu Lys Gln Ala Gln Lys Asn Leu Arg Arg
 180 185

50 (2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Lys Leu Pro Gly Lys Phe Arg Arg Ala His Gln Gly Asn Leu Glu
 1 5 10 15

601

Ser Gln Leu Thr Ser Glu Ser Tyr Tyr Lys Glu Thr Leu Ser Val Pro
 20 25 30
 5 Thr Val Glu His Ile Ile Gln Glu Leu Lys Asp Ile Phe Ser Glu Gln
 35 40 45
 His Leu Lys Ala Leu Lys Cys Leu Ser Leu Val Pro Ser Val Met Gly
 50 55 60
 10 Gln Leu Lys Phe Asn Thr Ser Glu Glu His His Ala Asp Met Tyr Arg
 65 70 75 80
 Ser Asp Leu Pro Asn Pro Asp Thr Leu Ser Ala Glu Leu His Cys Trp
 85 90 95
 15 Arg Ile Lys Trp Lys His Arg Gly Lys Asp Ile Glu Leu Pro Ser Thr
 100 105 110
 Ile Tyr Glu Ala Leu His Leu Pro Asp Ile Lys Phe Phe Pro Asn Val
 115 120 125
 Tyr Ala Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu
 130 135 140
 25 Asn Glu Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg
 145 150 155 160
 Asn Thr Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile
 165 170 175
 30 Asn Phe Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile
 180 185 190
 Lys Leu Tyr Thr Xaa Xaa Ser Xaa Leu Xaa Thr Xaa Xaa Ser Xaa Xaa
 195 200 205
 Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 210 215 220
 40 Asp Xaa Xaa Xaa Arg Glu Lys Ala Val Arg Cys Met Xaa
 225 230 235

45 (2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Lys Pro Met Ala Val Val Ala Ser Thr Val Leu Gly Leu Val Gln
 1 5 10 15
 55 Asn Met Arg Ala Phe Gly Gly Ile Leu Val Val Val Tyr Tyr Val Phe
 20 25 30
 Ala Ile Ile Gly Ile Asn Leu Phe Arg Gly Val Ile Val Ala Leu Pro
 35 40 45

Gly Asn Ser Ser Leu Ala Pro Ala Asn Gly Ser Ala Pro Cys Gly Ser
 50 55 60
 5 Phe Glu Gln Leu Glu Tyr Trp Ala Asn Asn Phe Asp Asp Phe Ala Ala
 65 70 75 80
 Ala Leu Val Thr Leu Trp Asn Leu Met Val Val Asn Asn Trp Gln Val
 85 90 95
 10 Phe Leu Asp Ala Tyr Arg Arg Tyr Ser Gly Pro Trp Ser Lys Ile Tyr
 100 105 110
 Phe Val Leu Trp Trp Leu Val Ser Ser Val Ile Trp Val Asn Leu Phe
 115 120 125
 15 Leu Ala Leu Ile Leu Glu Asn Phe Leu His Lys Trp Asp Pro Arg Ser
 130 135 140
 20 His Leu Gln Pro Leu Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr
 145 150 155 160
 Val Glu Leu Leu Phe Arg Asp Ile Leu Glu Glu Pro Gly Glu Asp Glu
 165 170 175
 25 Leu Thr Glu Arg Leu Ser Gln His Pro His Leu Trp Leu Cys Arg Xaa
 180 185 190

30

35 (2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Asn Val Val Val Val Ala Phe Gly Leu Ile Leu Ile Ile Glu Ser Leu
 1 5 10 15

45 Gly Glu Gln Cys Pro
 20

50 (2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
 1 5 10 15

60

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
 20 25 30

5 Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
 35 40 45

Ala Pro Xaa
 50

10

(2) INFORMATION FOR SEQ ID NO: 415:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

20 Met Leu Ile Ile Ser Leu Arg Pro Gln Phe Pro Ser Leu Ile Val Gln
 1 5 10 15

Leu Glu Cys Ser Val Leu Phe Leu Pro Ile Ser Leu Asn Leu Leu Leu
 20 25 30

25

30

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
 1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
 20 25 30

45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
 35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
 50 55 60

Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
 65 70 75 80

55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
 85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
 100 105 110

60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

604

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
 130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Ile Gly Arg Pro
 145 150 155 160

10 Gln Val Xaa

15 (2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
 1 5 10 15

25 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
 20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
 35 40 45

30 Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

35 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
 65 70 75 80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
 85 90 95

40 Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
 100 105 110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu
 115 120 125

45 Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro
 130 135 140

50 Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys
 145 150 155 160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu Xaa
 165 170

55

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

5 Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Val Ala Met Met
 1 5 10 15

Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala Leu Arg
 20 25 30

10 Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Cys Cys Leu
 35 40 45

Ala Xaa
 15 50

(2) INFORMATION FOR SEQ ID NO: 419:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Leu Gly Lys Gly Gly Gly Arg Ala Gly Leu Leu Arg Tyr Arg Leu
 1 5 10 15

30 Leu Tyr Phe Thr Leu Val Val Gly Glu Gly Glu Pro Gly Glu Asn Lys
 20 25 30

Val Thr Ile Pro Phe Phe Glu Thr Gly Lys Lys Ile Ile Phe Cys Ser
 35 40 45

35 Val Lys Met Val Glu Asn Ser Asn Val Pro Ser His Lys Gly Pro Val
 50 55 60

40 Pro Leu Arg Ser Glu Gln Trp Glu Leu Lys Ile Ser Glu Thr Leu Gly
 65 70 75 80

Glu Gly Lys Ile Gly Phe Leu Leu Ile Gly Arg Cys Ser Ser Gly Xaa
 85 90 95

45 Gly Gly Leu Cys Phe Cys Trp Asp Val Leu Cys Cys Met Tyr Ala Tyr
 100 105 110

Met Asp Arg Ser Leu Leu Ser Leu
 115 120

50

(2) INFORMATION FOR SEQ ID NO: 420:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

606

Met Thr His Leu Leu Leu Thr Ala Thr Val Thr Pro Ser Glu Gln Asn
 1 5 10 15

5 Ser Ser Arg Glu Pro Gly Trp Glu Thr Ala Met Ala Lys Asp Ile Leu
 20 25 30

Gly Glu Ala Gly Leu His Phe Asp Glu Leu Asn Lys Leu Arg Val Leu
 35 40 45

10 Asp Pro Glu Val Thr Gln Gln Thr Ile Glu Leu Lys Glu Glu Cys Lys
 50 55 60

Asp Phe Val Asp Lys Ile Gly Gln Phe Gln Lys Ile Val Gly Gly Leu
 65 70 75 80

15 Ile Glu Leu Val Asp Gln Leu Ala Lys Glu Ala Glu Asn Glu Lys Met
 85 90 95

20 Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys Ser Ile Ala Lys Gln Arg
 100 105 110

Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu Ile Ala Glu Lys Lys Met
 115 120 125

25 Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu Ala Leu Cys Lys Val Glu
 130 135 140

Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe Ile Phe Gln Lys Xaa
 145 150 155

30

(2) INFORMATION FOR SEQ ID NO: 421:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15

45 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45

50 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80

55 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95

60 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110

607

Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125

5 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr Xaa
 145 150

10

(2) INFORMATION FOR SEQ ID NO: 422:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

20 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala Leu
 1 5 10 15

25 Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile Ala Ala
 20 25 30

Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val Val Gly Val
 35 40 45

30 Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala Leu Val Gly Leu
 50 55 60

Ile Gly Ala Val Lys His His Gln Val Leu Leu Phe Phe Tyr Met Ile
 65 70 75 80

35 Ile Leu Leu Leu Val Phe Ile Val Gln Phe Ser Val Ser Cys Ala Cys
 85 90 95

40 Leu Ala Leu Asn Gln Glu Gln Gln Gly Gln Leu Leu Glu Val Gly Trp
 100 105 110

Asn Asn Thr Ala Ser Ala Arg Asn Asp Ile Gln Arg Asn Leu Asn Cys
 115 120 125

45 Cys Gly Phe Arg Ser Val Asn Pro Asn Asp Thr Cys Leu Ala Ser Cys
 130 135 140

Val Lys Ser Asp His Ser Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu
 145 150 155 160

50 Tyr Ala Gly Glu Val Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe
 165 170 175

Ser Phe Thr Glu Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn
 180 185 190

Gln Lys Asp Pro Arg Ala Asn Pro Ser Ala Phe Leu
 195 200

60

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

10 Met Leu Gln Ser Ile Ile Lys Asn Ile Trp Ile Pro Met Lys Pro Tyr
1 5 10 15
Tyr Thr Lys Val Tyr Gln Glu Ile Trp Ile Gly Met Gly Leu Met Gly
20 25 30
15 Phe Ile Val Tyr Lys Ile Arg Ala Ala Asp Lys Arg Ser Lys Ala Leu
35 40 45
Lys Ala Ser Ala Pro Ala Pro Gly His His Asn Gln Ile Tyr Leu Glu
20 50 55 60
Tyr Met Xaa
65

25

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

35 Met Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val
1 5 10 15
Ala Val Asn Asn Pro Lys Lys Gln Glu
20 25
40

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

50 Met Ala Ala Xaa Glu Pro Ala Val Leu Ala Leu Pro Asn Ser Gly Ala
1 5 10 15
Gly Gly Ala Gly Ala Pro Ser Gly Thr Val Pro Val Leu Phe Cys Phe
55 20 25 30
Ser Val Phe Ala Arg Pro Ser Ser Val Pro His Gly Ala Gly Tyr Glu
35 40 45
60 Leu Leu Ile Gln Lys Phe Leu Ser Leu Tyr Gly Asp Gln Ile Asp Met

609

	50		55		60
	His Arg Lys Phe Val Val Gln Leu Phe Ala Glu Glu Trp Gly Gln Tyr				
	65		70		75 80
5	Val Asp Leu Pro Lys Gly Phe Ala Val Ser Glu Arg Cys Lys Val Arg				
		85		90	95
10	Leu Val Pro Leu Gln Ile Gln Leu Thr Thr Leu Gly Asn Leu Thr Pro				
		100		105	110
	Ser Ser Thr Val Phe Phe Cys Cys Asp Met Gln Glu Arg Phe Arg Pro				
		115		120	125
15	Ala Ile Lys Tyr Phe Gly Asp Ile Ile Ser Val Gly Gln Arg Leu Leu				
		130		135	140
	Gln Gly Ala Arg Ile Leu Gly Ile Pro Val Ile Val Thr Glu Gln Tyr				
		145		150	155 160
20	Pro Lys Gly Leu Gly Ser Thr Val Gln Glu Ile Asp Leu Thr Gly Val				
		165		170	175
25	Lys Leu Val Leu Pro Lys Thr Lys Phe Ser Met Val Leu Pro Glu Val				
		180		185	190
	Glu Ala Ala Leu Ala Glu Ile Pro Gly Val Arg Ser Val Val Leu Phe				
		195		200	205
30	Gly Val Glu Thr His Val Cys Ile Gln Gln Thr Ala Leu Glu Leu Val				
		210		215	220
	Gly Arg Gly Val Glu Val His Ile Val Ala Asp Ala Thr Ser Ser Arg				
		225		230	235 240
35	Ser Met Met Asp Arg Met Phe Ala Leu Glu Arg Leu Ala Xaa Xaa Gly				
		245		250	255
40	Ile Ile Val Thr Thr Ser Glu Ala Val Leu Leu Gln Leu Val Ala Asp				
		260		265	270
	Lys Asp His Pro Lys Phe Lys Glu Ile Gln Asn Leu Ile Lys Ala Ser				
		275		280	285
45	Ala Pro Glu Ser Gly Leu Leu Ser Lys Val Xaa				
		290		295	

50 (2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Arg Asp Leu Gly Thr Leu Leu Ser Pro Val Cys Ser
1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 427:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val Gln Thr Ala Ala Gln
 1 5 10 15
 Gln Val Ala Glu Asp Lys Phe Val Phe Asp Leu Pro Asp Tyr Glu Ser
 20 25 30
 Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu
 35 40 45
 Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met
 50 55 60
 Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala
 65 70 75 80
 Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro
 85 90 95
 Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly
 100 105 110
 Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly
 115 120 125
 Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys
 130 135 140
 Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln
 145 150 155 160
 Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val
 165 170 175
 Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg Leu Ala Gln Asn Pro
 180 185 190
 Xaa Phe Trp Xaa Thr Xaa
 195

50

(2) INFORMATION FOR SEQ ID NO: 428:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser

1 5 10 15
 Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Leu Trp Lys
 20 25 30
 5 Asn Arg Gly Gly Val Gly Arg Ser Val Met Ser Ala Val Glu Xaa
 35 40 45

10
 (2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

15
 20 Met Lys Lys Val Glu Glu Lys Arg Val Asp Val Asn Ser Ala Val Ala
 1 5 10 15
 Met Gly Glu Val Ile Leu Ala Val Cys His Pro Asp Cys Ile Thr Thr
 20 25 30
 25 Ile Lys His Trp Ile Thr Ile Ile Arg Ala Arg Phe Glu Glu Val Leu
 35 40 45
 Thr Trp Ala Lys Gln His Gln Gln Arg Leu Glu Thr Ala Leu Ser Glu
 50 55 60
 30 Leu Val Ala Asn Ala Glu Leu Leu Glu Glu Leu Ala Trp Ile Gln
 65 70 75 80
 Trp Ala Glu Thr Thr Leu Ile Gln Arg Asp Gln Glu Pro Ile Pro Gln
 85 90 95
 35 Asn Ile Asp Arg Val Lys Ala Leu Ile Ala Glu His Gln Thr Phe Met
 100 105 110
 40 Glu Glu Met Thr Arg Lys Gln Pro Asp Val Asp Arg Val Thr Lys Thr
 115 120 125
 Tyr Lys Arg Lys Asn Ile Glu Pro Thr His Ala Pro Phe Ile Glu Lys
 130 135 140
 45 Ser Arg Ser Gly Gly Arg Lys Ser Leu Ser Gln Pro Thr Pro Pro Pro
 145 150 155 160
 50 Met Pro Ile Leu Ser Gln Ser Glu Ala Lys Asn Pro Arg Ile Asn Gln
 165 170 175
 Leu Ser Ala Arg Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Gln
 180 185 190
 55 Arg Lys Leu Asn Asp Ala Leu Asp Arg Leu Glu Glu Leu Lys Glu Phe
 195 200 205
 60 Ala Asn Phe Asp Phe Asp Val Trp Arg Lys Lys Tyr Met Arg Trp Met
 210 215 220

612

Asn His Lys Lys Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys
 225 230 235 240
 5 Asp Gln Asp Gly Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu
 245 250 255
 Ala Ser Lys Phe Pro Thr Thr Lys Leu Glu Met Thr Ala Val Ala Asp
 260 265 270
 10 Ile Phe Asp Arg Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val
 275 280 285
 Ala Ala Leu His Pro Asn Lys Asp Ala Tyr Arg Pro Thr Thr Asp Ala
 290 295 300
 15 Asp Lys Ile Glu Asp Glu Val Thr Arg Gln Val Ala Gln Cys Lys Cys
 305 310 315 320
 Ala Lys Arg Phe Gln Val Glu Gln Ile Gly Glu Asn Lys Tyr Arg Phe
 325 330 335
 20 Phe Leu Gly Asn Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg
 340 345 350
 25 Ile Leu Arg Asn Arg Asp Gly Ser Arg Trp Trp Arg Met Asp Gly Leu
 355 360 365
 Gly Xaa
 30 370

(2) INFORMATION FOR SEQ ID NO: 430:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:
 40 Met Asn Val Lys Thr Phe Ser Xaa Asp His Met His Phe Leu Cys Cys
 1 5 10 15
 45 Leu Tyr Leu Arg Tyr Val Thr Phe Val Tyr Leu Asn Leu Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 431:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:
 Met Glu Pro His Leu Arg Cys Arg Val Thr Arg Val Arg Gly Ser Leu
 1 5 10 15
 60 Gly Asn Thr Gly Arg Trp Leu Leu

5 (2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met His Tyr Leu Val Leu Gly Gly Leu Gly Val Phe Leu Phe Phe Ser
 1 5 10 15
 Cys Phe Val Phe Leu Phe Phe Xaa Phe Ser Phe Ala Phe Phe Pro Phe
 20 25 30
 Tyr Leu Glu Gly Met Gly Gly Ser Gly Asn Arg Glu Val Gly Gly Gly
 20 35 40 45
 Phe Cys Leu Phe Phe
 50

25

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

35 Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg
 1 5 10 15
 Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
 20 25 30
 Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu
 35 40 45
 Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu
 45 50 55 60
 Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val
 65 70 75 80
 50 Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Ile Thr Gly Gly
 85 90 95
 Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu Met Met Asp Gly
 100 105 110
 55 His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly Arg Lys Arg Asn
 115 120 125
 60 Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu Ile Asn His Asp
 130 135 140

Val Trp Ser Pro Ser Thr Ser Arg Leu Thr Arg Tyr Thr Ile Trp His
 145 150 155 160

5 Leu Gln Pro Pro Leu Gln Thr Thr Cys Ile Ile Leu Ser Arg His Xaa
 165 170 175

10

(2) INFORMATION FOR SEQ ID NO: 434:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

25

Met Leu Arg Cys Trp Pro Leu Phe Trp Leu Pro Leu Val Ser Pro Phe
 1 5 10 15

25

Cys Ser Leu Phe Trp Leu Leu Val Glu Trp Phe Gly Thr Asn Ile Asp
 20 25 30

30

Arg Glu Ser Tyr Asp Ala Ile Gly Gly Pro Ser Trp Met Thr Ala Ser
 35 40 45

35

Ser Phe Cys Leu Ser Asn Ser Asn Ile Trp Ser Leu Glu Ile Ser Ser
 50 55 60

Gly Ser Thr Ser Val Val His Ser Gln Gln Ala Met Asp
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 435:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

50

Met Arg Ser Cys Glu Ile Gln Leu Cys Val Trp Leu Leu Val Ser Ser
 1 5 10 15

His Val Asp Met Val Leu Gly Gly Ser Pro Ser Thr Leu Tyr Met Met
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 436:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

5 Met Val Val Asn Ser Leu Cys Phe Leu Ser Leu Leu Val Ile Leu
 1 5 10 15
 Glu Leu Ser Thr Asp Ser Ser Ala Arg Leu Leu Tyr His Glu
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 437:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

20

Met Asp Lys Gln Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile
 1 5 10 15

25

Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser
 20 25 30

Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val
 35 40 45

30

Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg
 50 55 60

Glu Phe Gly Asp Gln
 65

35

(2) INFORMATION FOR SEQ ID NO: 438:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

45

Met Pro Leu Cys Phe Phe Ser Phe Leu Cys Cys Trp Val Leu Val Phe
 1 5 10 15

Lys Leu Ile

50

(2) INFORMATION FOR SEQ ID NO: 439:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15
 5 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30
 Arg Val Met Val Asn Leu Asn Ile Leu Phe Xaa
 35 40
 10

(2) INFORMATION FOR SEQ ID NO: 440:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:
 20 Met Leu Leu Phe Pro Ser Leu Leu Phe Ala Ala Thr Tyr Asn Val Ala
 1 5 10 15
 25 Asn Pro Ser Arg Leu Ile Leu Tyr Met Ile Ser Ala Gly Ala Asp Ser
 20 25 30
 Gln

30

(2) INFORMATION FOR SEQ ID NO: 441:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:
 40 Met Trp Gln Val Arg Gly Leu Pro Pro Val Pro Leu Leu Leu Thr Met
 1 5 10 15
 Ser Pro Pro Pro Cys Leu Ser Ser Pro Phe Pro Phe Ile Ser Val Pro
 20 25 30
 45 Leu Phe Glu Ala Val Pro Ile Ser Val Ser Asp Gln Pro Ser Pro Xaa
 35 40 45
 50 Leu Thr Thr Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO: 442:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ile Thr Ser Val Leu Val Phe Leu Ile Phe Phe Phe Pro Tyr Leu
 1 5 10 15
 5 Ser Leu Val Thr Leu Leu Gln Ala Arg Asn Leu Trp Val Ile His Arg
 20 25 30
 Ala Ala Leu Cys Glu Ser Gly Leu Phe His Trp Arg Lys Gly Ile Glu
 35 40 45
 10 Asn Gln Leu Glu Pro Met Tyr Phe Leu Pro His Gly Thr Leu Phe Leu
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 443:
 20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Leu Tyr Ser Cys Glu Pro Tyr Leu Ile Ile Leu Asn Ile Tyr Ser
 1 5 10 15
 30 Gln Lys Ala Phe Tyr Phe Tyr Phe Phe Glu Gly Ser Phe Ser Val Cys
 20 25 30
 Thr Leu

35

(2) INFORMATION FOR SEQ ID NO: 444:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Arg Gln Arg Gln Ala Ala Cys Gln Pro Pro Pro Ser Arg Asn Gly
 1 5 10 15
 50 Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 20 25 30
 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Ser Ser Pro Leu
 35 40 45
 55 Asn Leu Leu Leu Leu Val Ser Ile Ser Trp Asp Leu Gly Leu Lys Leu
 50 55 60
 Asn Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr
 65 70 75 80

60

Lys Lys Phe Asn Lys Lys Lys Lys
85

5

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

15

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

20

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

25

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

30

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

35

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

40

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

45

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

50

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

55

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

60

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270

5 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Pro Pro Gly Pro Glu Lys Ser
 290 295 300

10 Gly Asn Pro Arg Thr Pro Ser Thr Leu Thr Ser Gln Gly Gln Gly Arg
 305 310 315 320

15 Glu Ala Ala Leu Leu Gly Leu Leu Thr Leu Gln Gly Thr Val Ala Phe
 325 330 335

Val Glu Thr Leu Met Glu Ile Cys Leu Thr Ser Gly Lys Asp
 340 345 350

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Val Phe Leu Pro Arg Gly Val Val Val Ser Gly Gly Ala Ala Cys
 1 5 10 15

Leu Trp Leu Thr Phe Ile Leu Glu Thr Glu Val Tyr Leu Asp Leu Ala
 20 25 30

35 Thr Glu Ala Arg Ala His Ser Arg Met Gly Leu Gly Leu Trp Pro Pro
 35 40 45

40 Asn

45 (2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp Gln Pro
 1 5 10 15

55 Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu Ala Glu
 20 25 30

Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys Lys Asp
 35 40 45

60

620

Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly Cys Ile
 50 55 60
 Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser Glu Ser
 5 65 70 75 80
 Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu Glu Leu
 85 90 95
 10 Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His Val Phe
 100 105 110
 Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu Leu Gln
 115 120 125
 15 Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe Asp Ser
 130 135 140
 Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu Ala Ala
 20 145 150 155 160
 Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu Leu Val Ala
 165 170 175
 25 Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro Ile Thr
 180 185 190
 Ala Xaa Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala Gly Ser
 195 200 205
 30 Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val Val Leu
 210 215 220
 Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg Arg Val
 35 225 230 235 240
 Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser His Leu
 245 250 255
 40 Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe Met Arg
 260 265 270
 Asn Cys Val Arg Cys Xaa
 275

(2) INFORMATION FOR SEQ ID NO: 448:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu
 1 5 10 15
 60 Gln Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly
 20 25 30

621

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
 35 40 45
 5 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
 50 55 60
 Thr Ile Ala Gly Met Thr Phe Thr Thr Phe Asp Leu Gly Gly His Val
 65 70 75 80
 10 Gln Ala Arg Arg Val Trp Lys Asn Tyr Leu Pro Ala Ile Asn Gly Ile
 85 90 95
 Val Phe Leu Val Asp Cys Ala Asp His Glu Arg Leu Leu Glu Ser Lys
 100 105 110
 15 Glu Glu Leu Asp Ser Leu Met Thr Asp Glu Thr Ile Ala Asn Val Pro
 115 120 125
 20 Ile Leu Ile Leu Gly Asn Lys Ile Asp Arg Pro Glu Ala Ile Ser Glu
 130 135 140
 Glu Arg Leu Arg Glu Met Phe Gly Leu Tyr Gly Gln Thr Thr Gly Lys
 145 150 155 160
 25 Gly Ser Ile Ser Leu Lys Glu Leu Asn Ala Arg Pro Leu Glu Val Phe
 165 170 175
 30 Met Cys Ser Val Leu Lys Arg Gln Gly Tyr Gly Glu Gly Phe Arg Trp
 180 185 190
 Met Ala Gln Tyr Ile Asp Xaa
 195

35

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:
 40 Met Thr Leu Ser Arg Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser
 1 5 10 15
 Tyr Asn Ile Leu Asp Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys
 20 25 30
 50 Glu Leu Thr Ala Leu Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro
 35 40 45
 His Arg Thr Val Lys Glu Lys Leu Pro His Met Val Glu Trp Trp Thr
 50 55 60
 Lys Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile
 65 70 75 80
 60 Ala Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys

622

85 90 95

Thr Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe
100 105 110

5 Ser Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys
115 120 125

Val Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn
10 130 135 140

Glu Asp Gly Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr
145 150 155 160

15 Asn Lys Asn Ser Ser Val Cys Glu Asn Xaa Gly Tyr Phe Gln Gln Leu
165 170 175

Glu Gly Lys Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu
20 180 185 190

Thr Met Ala Asp Gly Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly
195 200 205

25 Phe Leu Asn Asp Lys Val Glu Glu Arg Arg Xaa Arg Tyr Met Asp Ser
210 215 220

Tyr Asp Ile Val Leu Glu Lys Asp Glu Thr Leu Asp Val Val Asn Gly
225 230 235 240

30 Leu Leu Gln His Ile Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly
245 250 255

Pro Xaa

35

(2) INFORMATION FOR SEQ ID NO: 450:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

45

Met Ser His Val Leu Leu Cys Pro Ser Leu Ser Cys Ser Asn Leu Leu
1 5 10 15

50

Pro Pro Ser His Ser Leu Gly Thr Met Gly Ser Leu Ser Pro His Leu
20 25 30

Cys Gly His Thr Met Cys Pro Val Asn Pro Glu Leu Pro Leu Ser Ser
35 40 45

55

Arg Leu Thr Thr Asp Gln Pro Gln Pro Asp Ala Cys Ser Pro Thr Leu
50 55 60

60

Leu Thr Leu Pro Leu Pro Ser Ser Phe Leu Pro His Ser Lys Pro Thr
65 70 75 80

Phe Xaa His Pro Cys Ser Pro
85

5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

10 Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser
1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Xaa Pro Met Ala Ile
20 25 30

20 Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser
35 40 45

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp
50 55 60

25 Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn
65 70 75 80

30 Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala
85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile
100 105 110

35 Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly
115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln
130 135 140

40 Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe
145 150 155 160

45 Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His
165 170 175

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
180 185 190

50 Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
195 200 205

Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp
210 215 220

55 Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
225 230 235 240

60 Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
245 250 255

Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His
 260 265 270

5 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala
 275 280 285

Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe
 290 295 300

10 Cys Pro Glu Lys Val Ala Leu Ala Glu Ala Xaa
 305 310 315

15 (2) INFORMATION FOR SEQ ID NO: 452:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

20 Met Pro Gly Leu Ser Leu Ala Leu Leu Pro Phe Gly Pro Gly Cys Thr
 1 5 10 15

Glu Ala Leu His Ala Gly Cys Phe Pro Ala Phe Ala Ser Ala Thr Arg
 20 25 30

30 Val Asn Gly Glu Ala Ala Leu Ser Pro Gly Leu Cys Asp Pro Ile Ser
 35 40 45

Val Pro Tyr Val
 50

35 (2) INFORMATION FOR SEQ ID NO: 453:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

40 Met Ala Val Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys
 1 5 10 15

Gly Phe Ile Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val
 20 25 30

Leu Leu Trp Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala
 35 40 45

55 Gly Leu Lys Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys
 50 55 60

Asp Thr Glu Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys
 65 70 75 80

60

625

Asp Ser Asn Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala
 85 90 95
 5 Ser Gln Met Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser
 100 105 110
 Tyr Tyr Asn Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu
 115 120 125
 10 Tyr Met Thr Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr
 130 135 140
 Thr Gln Gly Leu Ser Gly Phe His Pro Gln Tyr Phe Asp Gly Ser Ile
 145 150 155 160
 15 Ser Tyr Asn Trp Asn Asn Gly Asn Cys Ser Phe Tyr Leu Ala Thr Ser
 165 170 175
 Lys Met Trp Phe Gly Ser Ala Gly Leu Ile Ser Gly Leu Ala Gln Leu
 180 185 190
 Ser Cys Leu Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro
 195 200 205
 25 Leu Asp Leu Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile
 210 215 220
 Gln Gly Glu Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu
 225 230 235 240
 30 Ile Tyr Met Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr
 245 250 255
 Ser Pro Glu Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly
 260 265 270
 Val Ile Ala Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr
 275 280 285
 40 Gln Leu Leu Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn
 290 295 300
 Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile
 305 310 315 320
 45 Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu
 325 330 335
 Ile Ser Val Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe
 340 345 350
 Ala Gln Asn Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala
 355 360 365
 55 Lys Glu Val Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val Xaa
 370 375 380
 60 (2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

5 Met Arg Ser Ile Gly Asn Lys Asn Thr Ile Leu Leu Gly Leu Gly Phe
 1 5 10 15
 10 Gln Ile Leu Gln Leu Ala Trp Tyr Gly Phe Gly Ser Glu Pro Trp Met
 20 25 30
 15 Met Trp Ala Ala Gly Ala Val Ala Ala Met Ser Ser Ile Thr Phe Pro
 35 40 45
 Ala Val Ser Ala Leu Val Ser Arg Thr Ala Asp Ala Asp Gln Gln Gly
 50 55 60
 20 Val Val Gln Gly Met Ile Thr Gly Ile Arg Gly Leu Cys Asn Gly Leu
 65 70 75 80
 Gly Pro Ala Leu Tyr Gly Phe Ile Phe Tyr Ile Phe His Val Glu Leu
 85 90 95
 25 Lys Glu Leu Pro Ile Thr Gly Thr Asp Leu Gly Thr Asn Thr Ser Pro
 100 105 110
 30 Gln His His Phe Glu Gln Asn Ser Ile Ile Pro Gly Pro Pro Phe Leu
 115 120 125
 Phe Gly Ala Cys Ser Val Leu Leu Ala Leu Leu Val Ala Leu Phe Ile
 130 135 140
 35 Pro Glu His Thr Asn Leu Ser Leu Arg Ser Ser Ser Trp Arg Lys His
 145 150 155 160
 Cys Gly Ser His Ser His Pro His Asn Thr Gln Ala Pro Gly Glu Ala
 165 170 175
 40 Lys Glu Pro Leu Leu Gln Asp Thr Asn Val
 180 185

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

50 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 1 5 10 15
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 20 25 30
 60 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

627

35 40 45

Val Leu Phe Asn Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
50 55 60

5 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
65 70 75 80

10 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
85 90 95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
100 105 110

15 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
115 120 125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
130 135 140

20 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
145 150 155 160

Arg Arg Xaa

25

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Ile Gln Val Phe Ile Leu Leu Leu Gly Ala Gly Gly Thr Ser
1 5 10 15

40 Gln Phe Thr Lys Pro Pro Ser Leu Pro Leu Glu Pro Glu Pro Ala Val
20 25 30

Glu Ser Ser Pro Thr Glu Thr Ser Glu Gln Ile Arg Glu Lys
35 40 45

45

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ser Tyr Leu Ala Phe Leu Tyr Met Thr Phe Asp Phe Cys Cys Leu
1 5 10 15

60 Tyr Phe Ser Thr Val Tyr Ala Pro Ser Phe Lys Tyr Ile Cys Val His
20 25 30

Thr Asp Thr His Ile Cys Val Cys Val Cys Ile Tyr Leu Ser Ser Val
 35 40 45

5 Val Ser Lys Ser Ser Ala Glu Ala Asp Gly Val Leu Gln Pro Arg Arg
 50 55 60

His Pro Ala Ser Leu Leu Ile Val Phe Ala Thr Ser Ile Ser Glu Ser
 65 70 75 80

10 Ser Leu Leu Ile Phe Ser Phe Gln Lys Thr Glu Ala Lys Leu Ile Val
 85 90 95

15 Phe Ala Val Ser Leu Ala Ala Lys Xaa
 100 105

20 (2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15

30 Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30

Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45

35 Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60

40 Ala His Thr Val Ala Xaa
 65 70

45 (2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15

55 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30

Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45

60

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60
 5 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
 65 70 75 80
 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95
 10 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110
 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 115 120 125
 15 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140
 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 145 150 155
 20

(2) INFORMATION FOR SEQ ID NO: 460:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
 1 5 10 15
 35 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 40 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 50 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 55 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 60

630

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175

5 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190

Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205

10 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220

Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 15 225 230 235 240

Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255

20 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270

Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285

25 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300

Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 30 305 310 315 320

Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 461:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

45 Met Leu Lys Cys Ile
 1 5

50 (2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ile Leu Thr Leu Leu Ser Val Val Ser Thr Met Ala Ser
 1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 463:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

10 Met Lys Leu His Pro Pro Pro Pro Ser Pro Val Thr Gln Asp His Arg
 1 5 10 15

15 Ser Lys Ser Ser His Ser Asn Trp Met Pro Arg Met Gly Ala Cys Ser
 20 25 30

Met Ser Arg Thr Ser Ser Ser Gly Pro Pro Ser Leu Cys Lys Ser Thr
 35 40 45

20 Ser Gly Arg Ser Cys Thr Arg Pro His Cys Trp Pro Ser Leu Pro Ala
 50 55 60

Trp Val Ser Val Phe Thr Arg Thr Asn Thr Gly Ser Trp Cys Tyr Pro
 65 70 75 80

25 Ala Trp Gly Gly Ala Phe Ser Arg Pro Trp Met Ser Ala Gln Ser Met
 85 90 95

30 Cys Cys Ala Glu Arg Ser Val Leu Gln Val Ala Cys Arg Leu Leu Asp
 100 105 110

Ala Leu Glu Phe Leu His Glu Asn Glu Tyr Val His Gly Asn Val Thr
 115 120 125

35 Ala Glu Asn Ile Phe Val Asp Pro Glu Asp Gln Ser Gln Val Thr Leu
 130 135 140

Ala Gly Tyr Gly Phe Ala Phe Arg Tyr Cys Pro Ser Gly Lys His Val
 145 150 155 160

40 Ala Tyr Val Glu Gly Ser Arg Ser Pro His Glu Gly Asp Leu Glu Phe
 165 170 175

45 Ile Ser Met Asp Leu His Lys Gly Cys Gly Pro Ser Arg Arg Xaa Asp
 180 185 190

Leu Gln Ser Leu Gly Tyr Cys Met Leu Lys Trp Leu Tyr Gly Phe Leu
 195 200 205

50 Pro Trp Thr Asn Cys Leu Pro Xaa Xaa Glu Asp Ile Met Lys Gln Lys
 210 215 220

Gln Lys Phe Val Asp Lys Pro Gly Pro Phe Val Gly Pro Cys Gly His
 225 230 235 240

55 Trp Ile Arg Pro Ser Glu Thr Leu Gln Lys Tyr Leu Lys Val Val Met
 245 250 255

60 Ala Leu Thr Tyr Glu Glu Lys Pro Pro Tyr Ala Met Leu Arg Asn Asn
 260 265 270

Leu Glu Ala Leu Leu Gln Asp Leu Arg Val Ser Pro Tyr
 275 280 285

5

(2) INFORMATION FOR SEQ ID NO: 464:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

15

Met Thr Ser Pro Pro Pro His Gln Gly Trp Glu Gln Arg Gly Cys Gly
 1 5 10 15

Glu Ser Gln Val Pro Leu Ala Leu Ser Arg Val Phe Ser Thr Ser His
 20 25 30

20

Tyr Cys Leu Leu Leu Val Ala Asn Gln Ser Ile Phe Phe Pro Cys Leu
 35 40 45

25

Trp Ala Val Glu Arg Leu Leu Gly Val Arg Cys Thr Cys Pro Leu Ser
 50 55 60

Trp Gly Lys Arg Ile Ile Ser Glu His Cys Ser Ala Gln Ser Ser Xaa
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met His Thr Trp Tyr Asn Asp Arg Arg Gln Asn Cys His Cys Leu Leu
 1 5 10 15

45

Phe Phe Leu Ile Tyr Leu Arg Lys Ile Tyr Gln Val Val Pro His Val
 20 25 30

50

Pro Leu Leu Val Lys Cys Arg Gly Arg Leu Lys Gly Val Asn Ile
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val
 1 5 10 15
 5 Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr
 20 25 30
 Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu
 35 40 45
 10 Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser
 50 55 60
 Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu
 15 65 70 75 80
 Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn Xaa
 85 90 95
 20

25 (2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Ala Ser Gly Ala Asp Ser Lys Gly Asp Asp Leu Ser Thr Ala Ile
 1 5 10 15
 35 Leu Lys Gln Lys Asn Arg Pro Asn Arg Leu Ile Val Asp Glu Ala Ile
 20 25 30
 Asn Glu Asp Asn Ser Val Val Ser Leu Ser Gln Pro Lys Met Asp Glu
 40 35 40 45
 Leu Gln Leu Phe Arg Gly Asp Thr Val Leu Leu Lys Gly Lys Lys Arg
 50 55 60
 45 Arg Glu Ala Val Cys Ile Val Leu Ser Asp Asp Thr Cys Ser Asp Glu
 65 70 75 80
 Lys Ile Arg Met Asn Arg Val Val Arg Asn Asn Leu Arg Val Arg Leu
 85 90 95
 50 Gly Asp Val Ile Ser Ile Gln Pro Cys Pro Asp Val Lys Tyr Gly Lys
 100 105 110
 Arg Ile His Val Leu Pro Ile Asp Asp Thr Val Glu Gly Ile Thr Gly
 55 115 120 125
 Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg
 130 135 140
 60 Pro Ile Arg Lys Gly Asp Ile Phe Leu Val Arg Gly Gly Met Arg Ala

634

145 150 155 160
 Val Glu Phe Lys Val Val Glu Thr Asp Pro Ser Pro Tyr Cys Ile Val
 165 170 175
 5 Ala Pro Asp Thr Val Ile His Cys Glu Gly Glu Pro Ile Lys Arg Glu
 180 185 190
 10 Asp Glu Glu Glu Ser Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly
 195 200 205
 Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu Met Val Glu Leu Pro Leu
 210 215 220
 15 Arg His Pro Ala Leu Phe Lys Ala Ile Gly Val Lys Pro Pro Arg Gly
 225 230 235 240
 Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Ile Ala Arg
 245 250 255
 20 Ala Val Ala Asn Glu Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro
 260 265 270
 25 Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys
 275 280 285
 Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ala Ile Ile Phe Ile Asp
 290 295 300
 30 Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val
 305 310 315 320
 Glu Arg Arg Ile Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys
 325 330 335
 35 Gln Arg Ala His Val Ile Val Met Ala Ala Thr Asn Arg Pro Asn Ser
 340 345 350
 40 Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp
 355 360 365
 Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu Glu Ile Leu Gln Ile His
 370 375 380
 45 Thr Lys Asn Met Lys Leu Ala Asp Asp Val Asp Leu Glu Gln Xaa
 385 390 395

50 (2) INFORMATION FOR SEQ ID NO: 468:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 1 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

 Leu

 1

60

(2) INFORMATION FOR SEQ ID NO: 469:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

10 Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1 5 10 15

15 Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
 20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
 35 40 45

20 His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
 50 55 60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
 65 70 75 80

25 Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
 85 90 95

30 Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110

Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125

35 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140

Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160

40 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175

Ile Val Ile Phe Xaa Ser Lys Pro Arg Asn Pro Arg Tyr Ala Pro His
 180 185 190

Leu Glu Pro Gly Ala Leu Pro Asn Leu Xaa Xaa Xaa Ser Leu Ser Lys
 195 200 205

50 Met Ser Xaa Xaa Ser Xaa Met Arg Asn Ser Gln Ala His Arg Asn Phe
 210 215 220

Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn
 225 230 235 240

55 Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu
 245 250 255

Leu Trp Ile Cys Cys Ala Thr Cys Cys Tyr Thr Leu Leu Asp Ala Val
 260 265 270

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 470:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

15 Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser
 1 5 10 15
 Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro
 20 25 30
 20 Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala
 35 40 45
 25 Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly
 50 55 60
 Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser
 65 70 75 80
 30 Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp
 85 90 95
 Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp
 100 105 110
 35 Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly
 115 120 125
 40 Xaa Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala
 130 135 140
 Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro
 145 150 155 160
 45 Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met
 165 170 175
 Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser
 180 185 190
 50

55

(2) INFORMATION FOR SEQ ID NO: 471:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

5 Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val Ser
 1 5 10 15
 Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
 20 25 30
 10 Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
 35 40 45
 Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
 50 55 60
 15 Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80
 20 Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95
 Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
 100 105 110
 25 Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125
 Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
 130 135 140
 30 Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160
 35 Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175
 Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190
 40 Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
 195 200 205
 Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu
 210 215 220
 45 Phe Ala Val Thr Leu Arg Ser Phe Val Pro
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

60 Met Leu His Ile Leu Pro Leu Lys Ser Tyr Asp Phe Pro His Phe Ser
 1 5 10 15

	Leu	Met	Gly	Arg	Tyr	Arg	Cys	Ala	Ser	Leu	Leu	Phe	Cys	Phe	Leu	Leu
				20					25						30	
5	Leu	Phe	Phe	Phe	Phe	Cys	Ser	Val	Leu	Trp	Thr	Phe	Ser	Asp	Met	His
			35					40					45			
	Arg	Ser	Gly	Glu	Asp	Gly	Pro	Trp	Thr	Pro	Cys	Val	His	His	Leu	Ala
10		50					55					60				
	Ala	Ser	Leu	Ile	Ser	Tyr	Gly	Gln	Pro	Gly	Phe	Ile	Cys	Ile	Ser	Leu
	65					70					75					80
15	Phe	Ser	Pro	Val	Leu	Phe	Ile	Glu	Asn	Pro	Arg	His	Tyr	Ala	Asn	Ala
				85						90					95	
	Thr	Val	Thr	Thr	Leu	Gly	Asp	Trp	Xaa							
			100					105								

(2) INFORMATION FOR SEQ ID NO: 473:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

30 Met Val Phe Leu Lys Tyr Arg Phe Leu Phe Phe Leu Val Phe Leu Ala
1 5 10 15
Asn Cys Ile Tyr Ser Leu His Tyr Lys Pro Ser Leu Met Tyr Pro Lys
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

50 Met Ala Leu Ser Arg Gly Leu Pro Arg Glu Leu Ala Glu Ala Val Ala
1 5 10 15

Gly Gly Arg Val Leu Val Val Gly Ala Gly Gly Ile Gly Cys Glu Leu
20 25 30

55 Leu Lys Asn Leu Val Leu Thr Gly Phe Ser His Ile Asp Leu Ile Asp
35 40 45

Leu Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Gln
50 55 60

60

Lys Lys His Val Gly Arg Ser Lys Ala Gln Val Ala Lys Glu Ser Val
 65 70 75 80
 5 Leu Gln Phe Tyr Pro Lys Ala Asn Ile Val Ala Tyr His Asp Ser Ile
 85 90 95
 Met Asn Pro Asp Tyr Asn Val Glu Phe Phe Arg Gln Phe Ile Leu Val
 100 105 110
 10 Met Asn Ala Leu Asp Asn Arg Ala Ala Arg Asn His Val Asn Arg Met
 115 120 125
 Cys Leu Ala Ala Asp Val Pro Leu Ile Glu Ser Gly Thr Ala Gly Tyr
 130 135 140
 15 Leu Gly Gln Val Thr Thr Ile Lys Lys Gly Val Thr Glu Cys Tyr Glu
 145 150 155 160
 Cys His Pro Lys Pro Thr Gln Arg Thr Phe Pro Gly Cys Thr Ile Arg
 165 170 175
 20 Asn Thr Pro Ser Glu Pro Ile His Cys Ile Val Trp Ala Lys Tyr Leu
 180 185 190
 Phe Asn Gln Leu Phe Gly Glu Glu Asp Ala Asp Gln Glu Val Ser Pro
 195 200 205
 Asp Arg Ala Asp Pro Glu Ala Ala Trp Glu Pro Thr Glu Ala Glu Ala
 210 215 220
 30 Arg Ala Arg Ala Ser Asn Glu Asp Gly Asp Ile Lys Arg Ile Ser Thr
 225 230 235 240
 Lys Glu Trp Ala Lys Ser Thr Gly Tyr Asp Pro Val Lys Leu Phe Thr
 245 250 255
 35 Lys Leu Phe Lys Asp Asp Ile Arg Tyr Leu Leu Thr Met Asp Lys Leu
 260 265 270
 Trp Arg Lys Arg Lys Pro Pro Val Pro Leu Asp Trp Ala Glu Val Gln
 275 280 285
 Ser Gln Gly Glu Glu Thr Asn Ala Ser Asp Gln Gln Asn Glu Pro Gln
 290 295 300
 45 Leu Gly Leu Lys Asp Gln Gln Val Leu Asp Val Lys Ser Tyr Ala Arg
 305 310 315 320
 Leu Phe Ser Lys Ser Ile Glu Thr Leu Arg Val His Leu Ala Glu Lys
 325 330 335
 50 Gly Asp Gly Ala Glu Leu Ile Trp Asp Lys Asp Asp Pro Ser Ala Met
 340 345 350
 Asp Phe Val Thr Ser Ala Ala Asn Leu Arg Met His Ile Phe Ser Met
 355 360 365
 55 Asn Met Lys Ser Arg Phe Asp Ile Lys Ser Met Ala Gly Asn Ile Ile
 370 375 380
 60

640

Pro Ala Ile Ala Thr Thr Asn Ala Val Ile Ala Gly Leu Ile Val Leu
 385 390 395 400

5 Glu Gly Leu Lys Ile Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile
 405 410 415

Phe Leu Asn Lys Gln Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys
 420 425 430

10 Ala Leu Asp Pro Pro Asn Pro Asn Cys Tyr Val Cys Ala Ser Lys Pro
 435 440 445

Glu Val Thr Val Arg Leu Asn Val His Lys Val Thr Val Leu Thr Leu
 450 455 460

15 Gln Asp Lys Ile Val Lys Glu Lys Phe Ala Met Val Ala Pro Asp Val
 465 470 475 480

Gln Ile Glu Asp Gly Lys Gly Thr Ile Leu Ile Ser Ser Glu Glu Gly
 485 490 495

Glu Thr Glu Ala Asn Asn His Lys Lys Leu Ser Glu Phe Gly Ile Arg
 500 505 510

25 Asn Gly Ser Arg Leu Gln Ala Asp Asp Phe Leu Gln Asp Tyr Thr Leu
 515 520 525

Leu Ile Asn Ile Leu His Ser Glu Asp Leu Gly Lys Asp Val Glu Phe
 530 535 540

30 Glu Val Val Gly Asp Ala Pro Glu Lys Val Gly Xaa Lys Gln Ala Glu
 545 550 555 560

Asp Ala Ala Lys Ser Ile Thr Asn Gly Gln Xaa
 565 570

35

(2) INFORMATION FOR SEQ ID NO: 475:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu Thr His Cys
 1 5 10 15

50 Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu Arg Thr Pro
 20 25 30

Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe Gly Asn Lys
 35 40 45

55 Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser Ser Arg Val
 50 55 60

60 Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu Thr Phe Thr
 65 70 75 80

Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala Leu Ser Ile
 85 90 95
 5 Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro Pro Gly Cys
 100 105 110
 Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr Ser Ser Glu
 115 120 125
 10 Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu Pro Glu Phe
 130 135 140
 Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp Asp Gly Arg
 145 150 155 160
 15 Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln Thr Tyr Pro
 165 170 175
 20 Gln Pro Ser Pro Ser Ser Ser Met Thr Cys Lys Val Met Thr Ser Trp
 180 185 190
 Ala Val Ser Pro Trp Thr Thr Leu Gly Arg Cys Gln Val Ala Arg Leu
 195 200 205
 25 Glu Pro Ala Arg Ala Val Lys Ser Ser Gly Arg Cys Leu Ser Pro Val
 210 215 220
 Leu Arg Ala Glu Arg Ser Ser Ser Arg Cys Trp Leu Ala Ser Gly Arg
 225 230 235 240
 30 Pro Cys Val Ala Val Ser Cys Leu Ser Ser Ser Pro Ala Ser Pro Gly
 245 250 255
 35 His Ser Gln Pro Val Val Ser Ser Leu Thr Pro Thr Gly Ala Gly Gln
 260 265 270
 Gln Ala Phe Val Phe Ser Lys Asn Val Leu Ser Ser Leu Trp Tyr Leu
 275 280 285
 40 Asn Leu Thr Val Leu Ala Glu Asn Val Asn Met Cys Val Cys Cys Val
 290 295 300
 Asn Ser Phe Ser Cys Trp Glu Xaa
 305 310
 45

(2) INFORMATION FOR SEQ ID NO: 476:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp
 1 5 10 15

60

Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile

	20	25	30
	Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln		
	35	40	45
5	Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr		
	50	55	60
10	Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn		
	65	70	75 80
	Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile		
	85	90	95
15	Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn		
	100	105	110
	Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile		
	115	120	125
20	Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser		
	130	135	140
25	Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu		
	145	150	155 160
	Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn		
	165	170	175
30	Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr		
	180	185	190
	Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala		
	195	200	205
35	Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr		
	210	215	220
40	Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu		
	225	230	235 240
	Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Asp Ala Ala		
	245	250	255
45	Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr Gln		
	260	265	270
	Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val Leu		
	275	280	285
50	Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln Phe		
	290	295	300
55	Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro Gly		
	305	310	315 320
	Thr Ser Ser Tyr Glu Ile Val Ile Xaa		
	325		
60			

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

10 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
1 5 10 15

Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
20 25 30

15 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
35 40 45

20 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
50 55 60

Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
65 70 75 80

25 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
85 90 95

Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
100 105 110

30 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
115 120 125

35 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
130 135 140

Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
145 150 155 160

40 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
165 170 175

Ala Xaa

45

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

55

Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val
1 5 10 15

Ile Leu Gly Leu Leu Cys Leu Leu Leu Cys Gly Gly Gly Glu Gly Lys
20 25 30

60

Val Ala Gly Arg Gln Ala Val Thr Ser Asp Gln Gln Ser Val Gly Arg
 35 40 45

5 Arg Asp Val Tyr
 50

10 (2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Gln Lys Lys Asn Ser Leu Phe Phe Phe Phe Ala Phe Tyr Tyr Glu
 1 5 10 15

20 Asn Lys Thr Asn Ala Pro Gly Glu Gly Ser Met Ile Thr Arg Asn Ile
 20 25 30

25 Lys Glu Tyr Phe Leu Pro Phe Leu Phe Cys Cys Val Glu Ala Ser Ile
 35 40 45

Ala Ile Asn Lys Leu Asn Tyr Leu His Trp Thr His Phe Gln
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

40 Met Pro Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
 1 5 10 15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25

45

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

55 Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
 1 5 10 15

60 Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
 20 25 30

645

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
 35 40 45
 5 His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
 50 55 60
 Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
 65 70 75 80
 10 His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
 85 90 95
 Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
 100 105 110
 15 Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
 115 120 125
 Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Xaa Glu Gln
 130 135 140
 20 Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
 145 150 155 160
 25 Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
 165 170 175
 Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
 180 185 190
 30 Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
 195 200 205
 Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
 210 215 220
 35 Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
 225 230 235 240
 40 Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
 245 250 255
 Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
 260 265 270
 Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
 275 280 285
 50 Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
 290 295 300
 Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
 305 310 315 320
 55 Gly Arg Tyr Leu Gln Met Lys Ala Lys Xaa Gln Gly His Ala Xaa Xaa
 325 330 335
 Gln Pro Xaa
 60

5 (2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Leu Asn Ser Asn Ile Asn Asp Leu Leu Met Val Thr Tyr Leu Ala
1 5 10 15

15 Asn Leu Thr Gln Ser Gln Ile Ala Leu Asn Glu Lys Leu Val Asn Leu
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 483:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
1 5 10 15

35 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr Arg Ile Gly
20 25 30

Cys Phe Lys Thr Ile Thr Cys Trp Pro Thr Ser Leu Thr Gln Arg Xaa
35 40 45

40

45 (2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Tyr Met Tyr Ser Leu Asn Val Phe Leu Ser Phe Ile Phe Leu Ala
1 5 10 15

55 Leu Val Phe Lys Cys Val His Val Cys Gln Gly Ala Asn Ala Phe Leu
20 25 30

60 Phe Leu Lys Leu Val Phe
35

5 (2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Gly Leu Arg Leu Ile Cys Leu Glu Leu Thr Met Val Lys Ala Leu
 1 5 10 15
 Val Cys Glu Met Phe Leu Phe Phe Leu Met Thr Gln Lys Leu Ile Trp
 20 25 30
 Gln Glu Cys Thr Glu Lys Phe Ala Lys Leu Leu Val Gln Leu Ile Ser
 35 40 45
 Leu Val Phe Ala Trp Glu Phe Phe Ser Glu Asp Thr Pro
 50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 35 1 5 10 15
 Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30
 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45
 Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60
 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met
 45 65 70 75 80
 Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu
 50 85 90 95
 Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys
 100 105 110
 Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr
 55 115 120 125
 Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala
 130 135 140

60

648

Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp
 145 150 155 160
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu
 5 165 170 175
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala
 180 185 190
 10 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr
 195 200 205
 Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 15 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 20 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 25 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 30 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 35 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys Xaa.
 340 345

40

(2) INFORMATION FOR SEQ ID NO: 487:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

50 Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Arg Glu Gly Tyr Thr
 1 5 10 15
 Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Cys Met Leu
 20 25 30
 55 Ile Glu Leu Ala Leu Arg Gly Arg Leu Gln Leu Glu Ala Cys Gly Met
 35 40 45
 60 Arg Arg Lys Ser Leu Leu Thr Arg Lys Val Ile Cys Lys Ser Asp Ala
 50 55 60

Pro Thr Gly Asp Val Leu Leu Asp Glu Ala Leu Lys His Val Lys Glu
 65 70 75 80
 5 Thr Gln Pro Pro Glu Thr Val Gln Asn Trp Ile Glu Leu Leu Ser Gly
 85 90 95
 Glu Thr Trp Asn Pro Leu Lys Leu His Tyr Gln Leu Arg Asn Val Arg
 100 105 110
 10 Glu Arg Leu Ala Lys Asn Leu Val Glu Lys Gly Val Leu Thr Thr Glu
 115 120 125
 Lys Gln Asn Phe Leu Leu Phe Asp Met Thr Thr His Pro Leu Thr Asn
 130 135 140
 Asn Asn Ile Lys Gln Arg Leu Ile Lys Lys Val Gln Glu Ala Val Leu
 145 150 155 160
 20 Asp Lys Trp Val Asn Asp Pro His Arg Met Asp Arg Arg Leu Leu Ala
 165 170 175
 Leu Ile Tyr Leu Ala His Ala Ser Asp Val Leu Glu Asn Ala Phe Ala
 180 185 190
 25 Pro Leu Leu Asp Glu Gln Tyr Asp Leu Ala Thr Lys Arg Val Arg Gln
 195 200 205
 Leu Leu Asp Leu Asp Pro Glu Val Glu Cys Leu Lys Ala Asn Thr Asn
 210 215 220
 Glu Val Leu Trp Ala Val Val Ala Ala Phe Thr Lys Xaa
 225 230 235
 35

(2) INFORMATION FOR SEQ ID NO: 488:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:
 45 Met Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp
 1 5 10 15
 Ile Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser
 20 25 30
 50 Asp Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Ile Lys Gln Pro
 35 40 45
 Asp Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly
 50 55 60
 Lys Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln
 65 70 75 80
 60 Gln Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln Gln Thr Pro Pro

650

85 90 95
 Gly Leu Cys Pro Leu Ala Gly Asn Ser Val His Glu Asp Lys Lys Phe
 100 105 110
 5 Leu Asp Lys Tyr Met Pro Gln Phe Met Lys His Leu His Tyr Arg Ile
 115 120 125
 10 Ile Asp Val Ser Thr Val Lys Glu Leu Cys Arg Arg Trp Tyr Pro Glu
 130 135 140
 Glu Tyr Glu Phe Ala Pro Lys Lys Ala Ala Ser His Arg Ala Leu Asp
 145 150 155 160
 15 Asp Ile Ser Glu Ser Ile Lys Glu Leu Gln Phe Tyr Arg Asn Asn Ile
 165 170 175
 Phe Lys Lys Lys Ile Asp Glu Lys Lys Arg Lys Ile Ile Glu Asn Gly
 180 185 190
 20 Glu Asn Glu Lys Thr Val Ser Xaa
 195 200
 25
 (2) INFORMATION FOR SEQ ID NO: 489:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:
 30 Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly
 1 5 10 15
 Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala
 20 25 30
 40 Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu
 35 40 45
 Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala
 50 55 60
 45 Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu
 65 70 75 80
 Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln
 50 85 90 95
 Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
 100 105 110
 55 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
 115 120 125
 Val Arg Thr Gly Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
 130 135 140
 60

651

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 145 150 155 160
 5 Phe Thr Leu Val Ala Ile¹Leu Leu His Gly Met Lys Thr Ser Asp Thr
 165 170 175
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 180 185 190
 10 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 195 200 205
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 210 215 220
 15 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 225 230 235 240
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 245 250 255
 20 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 260 265 270
 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 275 280 285
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 290 295 300
 30 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 305 310 315 320
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 325 330 335
 35 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His Xaa
 340 345 350
 40

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

50 Met Arg Gly Ser Arg Gly Gly Trp Ala Gly Glu Met Ala Ala Ser Gly
 1 5 10 15
 Glu Ser Gly Thr Ser Gly Gly Gly Gly Ser Thr Glu Glu Ala Phe Met
 20 25 30
 55 Thr Phe Tyr Ser Glu Val Lys Gln Ile Glu Lys Arg Asp Ser Val Leu
 35 40 45
 60 Thr Ser Lys Asn Gln Ile Glu Arg Leu Thr Arg Pro Gly Ser Ser Tyr
 50 55 60

Phe Asn Leu Asn Pro Phe Glu Val Leu Gln Ile Asp Pro Glu Val Thr
 65 70 75 80
 5 Asp Glu Glu Ile Lys Lys Arg Phe Arg Gln Leu Ser Ile Leu Val His
 85 90 95
 Pro Asp Lys Asn Gln Asp Asp Ala Asp Arg Ala Gln Lys Ala Phe Glu
 100 105 110
 10 Ala Val Asp Lys Ala Tyr Lys Leu Leu Leu Asp Gln Glu Gln Lys Lys
 115 120 125
 Arg Ala Leu Asp Val Ile Gln Ala Gly Lys Glu Tyr Val Glu His Thr
 130 135 140
 15 Val Lys Glu Arg Lys Lys Gln Leu Lys Lys Glu Gly Lys Pro Thr Ile
 145 150 155 160
 20 Val Glu Glu Asp Asp Pro Glu Leu Phe Lys Gln Ala Val Tyr Lys Gln
 165 170 175
 Thr Met Lys Leu Phe Ala Glu Leu Glu Ile Lys Arg Lys Glu Arg Glu
 180 185 190
 25 Ala Lys Glu Met His Glu Arg Lys Arg Gln Arg Glu Glu Glu Ile Glu
 195 200 205
 Ala Gln Glu Lys Ala Lys Arg Glu Arg Glu Trp Gln Lys Asn Phe Glu
 210 215 220
 30 Glu Ser Arg Asp Gly Arg Val Asp Ser Trp Arg Asn Phe Gln Ala Asn
 225 230 235 240
 35 Thr Lys Gly Lys Lys Glu Lys Lys Asn Arg Thr Phe Leu Arg Pro Pro
 245 250 255
 Lys Val Lys Met Glu Gln Arg Glu Xaa
 260 265
 40

(2) INFORMATION FOR SEQ ID NO: 491:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

50 Asp Ser Met Pro Thr Cys Pro Leu Xaa Ala Ser Leu Glu Cys Gly Pro
 1 5 10 15
 Leu Leu Pro Val Arg Leu Cys Cys Leu
 20 25
 55

(2) INFORMATION FOR SEQ ID NO: 492:

60

653

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Asn Glu Tyr Arg Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu
 1 5 10 15

10 Lys Ser Leu Ser Phe Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp
 20 25 30

Tyr Ile Tyr Ala Val Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg
 35 40 45

15 Asp Leu Val His Arg Gln Thr Ala Ser Ala Val Val Gln His Met Ser
 50 55 60

Leu Gly Val Tyr Gly Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu
 20 65 70 75 80

Asn Tyr Val Trp Pro Asn Val Phe Glu Thr Ser Pro His Val Ile Gln
 85 90 95

25 Ala Val Met Gly Ala Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys
 100 105 110

Arg Met Leu Gln Tyr Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys
 115 120 125

30 Val Arg Asp Val Tyr Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser
 130 135 140

Gln Asp Ala Leu Ile Ala His Tyr Pro Arg Ile Tyr Gln Arg Xaa
 35 145 150 155

40 (2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ile Ser Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met
 1 5 10 15

50 Tyr Asp Gly Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln
 20 25 30

Leu Glu Asp Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala
 35 40 45

55 Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu
 50 55 60

Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr
 60 65 70 75 80

654

Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys
 85 90 95
 5 Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro
 100 105 110
 His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln
 115 120 125
 10 Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys
 130 135 140
 Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro
 15 145 150 155 160
 Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn
 165 170 175
 20 Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr
 180 185 190
 Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile
 195 200 205
 25 Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln
 210 215 220
 Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Xaa Ile Glu
 30 225 230 235 240
 Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn
 245 250 255
 35 Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val
 260 265 270
 Met Ile Gln Lys Pro Trp Xaa
 275
 40

(2) INFORMATION FOR SEQ ID NO: 494:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:
 50 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 55 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 60 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

655

[illegible]

30

(2) INFORMATION FOR SEQ ID NO: 495:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEO ID NO: 495:

40	Met	Ala	Ala	Gly	Asp	Gln	Val	Phe	Ser	Gly	Ala	Gly	His	Val	Xaa	Glu
	1				5					10					15	
	His	Val	Ala	Gly	Gly	Arg	His	Ala	Trp	Leu	Leu	Thr	Trp	Gln	Ser	Ala
				20					25					30		
45	Cys	Pro	Ala	Asn	Arg	Leu	Ser	Leu	Val	Pro	Leu	Val	Pro	Ser	Ala	Ser
			35				40						45			
	Met	Thr	Arg	Leu	Met	Arg	Xaa	Arg	Thr	Ala	Ser	Gly	Ser	Ser	Val	Ile
50		50					55					60				
	Leu	Trp	Met	Ala	Pro	Ala	Ala	Ala	Pro	Thr	Pro	Ala	Arg	Ala	Pro	Glu
	65					70					75					80
55	Ala	Ala	Pro	Thr	Pro	Ala	Arg	Ala	Pro	Ala	Ala	Ala	Arg	Thr	Pro	Ala
					85					90					95	
	Arg	Gly	Pro	Thr	Trp	Thr	Ser	Pro	Pro	Thr	Arg	Val	Leu	Leu	Gly	Thr
60				100					105					110		

656

Xaa Pro Gly Pro Ser Pro Trp Arg Ser Pro Ala Arg Arg Pro Ala Gln
 115 120 125
 5 Leu Pro Pro Pro Asp Ser Asp Leu Cys Ser Gly Pro Leu Leu Pro Gly
 130 135 140
 Pro Phe Ser Pro Pro Ala Cys His Thr Ala Pro Asn Ser Val Leu Ile
 145 150 155 160
 10 Gln Ser Leu Phe Cys Lys Ser Glu Leu Trp Trp Arg Gln Met Arg Ser
 165 170 175
 Ile Thr Trp Val Pro Ser Pro Lys Ala Gly Trp Arg Trp Thr Lys Gly
 180 185 190
 15 Arg Lys Gln Ala Ser Pro His Arg Ile Leu Phe His Xaa
 195 200 205
 20
 (2) INFORMATION FOR SEQ ID NO: 496:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 25 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:
 30 Met Ala Leu Thr Leu Leu Pro Ser Val Ser Arg Leu Pro Gly Glu Arg
 1 5 10 15
 Met Ala Ala Ser Gly Leu Pro Tyr Val Leu His His Lys Ser Ser Leu
 20 25 30
 35 Met Lys Val Ile Phe Phe Pro Tyr Pro Val Leu Pro Leu Pro Ala Pro
 35 40 45
 Asn Gly Thr Trp Val Pro Arg Leu Val Leu Gly Leu Gly Ser Gly Asp
 50 55 60
 40 Gln Val His Tyr Leu Pro Ile Ser Ser Ser Ile Val Asn Tyr Gly Thr
 65 70 75 80
 Ser Val Ser Gly Lys Ser Trp Val Phe Leu Val Tyr Pro Leu His Pro
 85 90 95
 45 Thr Pro Thr Trp Ser Thr Arg Cys Phe Gln Val Trp Asp Leu Leu Ser
 100 105 110
 50 Val Glu Leu Pro Asp Lys Gly Glu Gly Asn Thr Arg Arg Ala Ser Gly
 115 120 125
 Val Pro Gly Leu Ser Gln Leu Pro Thr Ser His Lys Pro Ile Lys Gln
 130 135 140
 55 Glu Tyr Xaa
 145
 60

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

5 Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 10 1 5 10 15
 Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys Glu Val Gly
 20 25 30
 15 Ala Ala Leu Pro Pro Arg Gly Pro Ser Leu Ser Asp Cys Leu Gly Leu
 35 40 45
 Pro Pro Trp Thr Pro Trp Gly Pro Ala Trp Thr Leu Ala Gln Ser Xaa
 20 50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

30 Met Ser Thr Gly Ala Leu Asn Thr Ser Pro Pro Ala Ser Asn Arg Leu
 35 1 5 10 15
 Glu Ser Thr Leu Asn Glu Tyr Leu Ile Gln Pro Gln Leu His Cys Ser
 20 25 30
 40 Ser Val Gln Arg Leu Thr Leu Lys Trp Gly Cys Ser Ser Leu Gln Arg
 35 40 45
 Asp Gly Gln Ala Val Pro Trp Gly Leu Trp Gln Arg Ala Tyr Pro Ser
 45 50 55 60
 Leu Leu Pro Thr Leu Pro Ser Asp Leu Leu Arg Pro His Ala Val Thr
 65 70 75 80
 50 Pro Ser Val Ser Val Ser Val His Thr Cys Glu Ser Ser Xaa
 85 90

55

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

60

658

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Xaa Leu Phe Ser Ser Ser
 1 5 10 15

5 Leu Pro Phe Leu Trp Leu
 20

10 (2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Arg Gly Gly Leu Cys Pro Leu Leu Val Pro Gly Pro Leu Ala Arg Gln
 1 5 10 15

20 Glu Pro Ser Pro Ser Leu Gln Gly Cys Ser Glu Ser Pro Val Gly Met
 20 25 30

25 Asp

30 (2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
 1 5 10 15

40 Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
 20 25

45 (2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Pro Gly Lys Pro Gln Ala Cys Pro Glu Leu Thr Ser Val Leu Pro
 1 5 10 15

55

(2) INFORMATION FOR SEQ ID NO: 503:

60 (i) SEQUENCE CHARACTERISTICS:

659

(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

5

Asn Lys Ser Leu Xaa Ser Cys Leu Phe Val Leu His Phe Val Leu His
1 5 10 15

Cys Xaa Phe

10

(2) INFORMATION FOR SEQ ID NO: 504:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Lys Thr His Arg Leu Arg Ile Arg Asn Pro Cys Leu Gln Phe
1 5 10 15

25

Ser Ile Leu Asn Leu Phe Leu Leu Lys Met Ile Val Ser
20 25

30

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln
1 5 10 15

40

Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu
20 25 30

45

Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly
35 40 45

Pro Ser Ser Phe Gln Asn Pro Ala Ser Ser Pro Ser Ser Trp Thr His
50 55 60

50

Glu Glu Glu Pro Gly Tyr Phe Pro Gln Tyr Xaa
65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Leu Pro Leu Ala Glu Leu Lys Asn Trp Val
1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 507:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

15

Met Leu Trp Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu
1 5 10 15

20

Ser Asp Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr
20 25 30

Gly Asp Val Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys
35 40 45

25

Thr Gly Val Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val
50 55 60

Ala Arg Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe
65 70 75 80

30

Met Met Asp Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg
85 90 95

35

Val Leu Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu
100 105 110

Ser His Ala Ala Arg Arg His Gln Arg Xaa Leu Leu Ala Ala Ile Asn
115 120 125

40

Ala Phe Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val
130 135 140

Asn Ser Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu
145 150 155 160

45

Gln Gln Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp
165 170 175

50

Thr Leu Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala
180 185 190

Leu Gly Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
195 200 205

55

(2) INFORMATION FOR SEQ ID NO: 508:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

661

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

5 Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15
 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Pro Ala
 20 25 30
 10 Val Xaa Lys Lys
 35

15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

25 Met Ala Leu Val Ala Leu Phe Thr Gln Leu Met Arg Xaa Leu Gly Arg
 1 5 10 15
 Cys Pro Gln

30

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

40 Met Thr Phe Pro Phe Glu Lys Glu Asn Ser Cys Phe Gln Cys Leu Leu
 1 5 10 15
 Phe Asp Ser Trp Arg Glu Gln Thr Arg Thr Asn Ile Gln Pro Gln Arg
 20 25 30
 45

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

60 Met His Leu Leu Asp Phe Phe Arg Asp Leu Val Leu Leu Val Leu Leu
 1 5 10 15

Ala Leu Leu Asp Ser Phe Trp Leu Glu Val Gln Lys
20 25

5

(2) INFORMATION FOR SEQ ID NO: 512:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

15

Met Cys Leu Ile His Phe Ile Lys Ile Ile Leu Val Phe Ile Leu Lys
1 5 10 15

Leu Trp Leu Tyr Ser Gln Lys Cys Pro Lys
20 25

20

(2) INFORMATION FOR SEQ ID NO: 513:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

30

Met Ile His Val His Glu Trp Asn Asp Gln Met Leu Met Val Tyr Ile
1 5 10 15

35

Phe Leu Tyr Pro Val Ser Ile Thr Phe Leu Asn Leu Cys Ser Leu Thr
20 25 30

Cys

40

(2) INFORMATION FOR SEQ ID NO: 514:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

50

Leu Asn Glu Ser Tyr Val Ser Arg Ala Gly Gly Trp Phe Ser Met Phe
1 5 10 15

Xaa Leu Ile Phe Phe Leu Leu Ala Leu Gly Ser Xaa Leu Cys Leu Leu
20 25 30

55

Leu Cys Leu Pro Ser Phe Asn Lys Thr Arg Arg Lys Gln Lys Pro
35 40 45

60

663

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5 Ser Ser Lys Thr Pro Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly Ser
 1 5 10 15

Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu Gly
 20 25 30

15 Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp
 35 40

20 (2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Leu Asn Trp
 1
 30

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

35 Phe Ala Phe Cys Ala Glu Leu Met Ile Gln Asn Trp Thr Leu Gly Ala
 1 5 10 15

45 Val Asp Ser Gln Met Asp Asp Met Asp Met Asp Leu Asp Lys Glu Phe
 20 25 30

Leu Gln Asp Leu Lys Glu Leu Lys Val Leu Val Ala Asp Lys Asp Leu
 35 40 45

50 Leu Asp Leu His Lys Ser Leu Val Cys Thr Ala Leu Arg Gly Lys Leu
 50 55 60

Gly Val Phe Ser Glu Met Glu Ala Asn Phe Lys Asn Leu Ser Arg Gly
 65 70 75 80

55 Leu Val Asn Val Ala Ala Lys Leu Thr His Asn Lys Asp Val Arg Asp
 85 90 95

60 Leu Phe Val Asp Leu Val Glu Lys Phe Val Glu Pro Cys Arg Ser Asp
 100 105 110

His Trp Pro Leu Ser Asp Val Arg Phe Phe Leu Asn Gln Tyr Ser Ala
 115 120 125

5 Ser Val His Ser Leu Asp Gly Phe Arg His Gln Ala Ser Gly Thr Ala
 130 135 140

Thr Trp Ala Pro Ser Ala Ala Ala Ser Cys Ala Cys Ile Met Thr Glu
 145 150 155 160

10 Val Pro Pro Asn Ala Pro Pro Thr Leu Thr Ile Lys Leu Leu
 165 170

15

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

20 Met Trp Lys Asn Leu Gly Ser Gly Ser Val Phe Val Thr Trp Phe Ser
 25 1 5 10 15

Leu Val Met Ile Leu Ser Gly Ile Gly Pro Leu Gly Asp Ala Glu Asp
 20 25 30

30 Ser Ile Ser Asp Val Ser His Arg Leu Arg Pro
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

40 Phe Gln Phe Pro Leu Leu Thr Ile Ala Leu Gln Phe Leu
 45 1 5 10

(2) INFORMATION FOR SEQ ID NO: 520:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

55

Met His Tyr Val Ile Val Leu Ser Leu Phe Val Val Leu Glu Lys Lys
 1 5 10 15

60

Asn Lys Met Gly Ser Asp Gly Cys Leu Arg Lys Asn Gly Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 521:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Arg Ser Ile Val Leu Arg Gly Ser Leu Phe Leu Phe Phe Ser
 1 5 10 15
 His Tyr Thr Leu Lys Leu Leu Ser Val Ile Lys Gln Thr Asn Arg Lys
 20 25 30
 Ile Val Trp Glu Lys Pro Cys Ile Arg Leu Phe Tyr Xaa Val Leu
 35 40 45

20

(2) INFORMATION FOR SEQ ID NO: 522:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Leu Pro Val Leu Leu Cys Leu Thr Leu Pro Met Pro Leu Pro
 1 5 10 15
 Ser Ala Thr Ala Arg Gly Gly Asn Arg Thr
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 523:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Ser Ser Ile Pro Val Ser Ile Leu Ile Gly Met Lys Leu Ile Leu Tyr
 1 5 10 15
 Leu Leu Ile Thr Glu Ser Gly Ser His Glu Lys Lys Ser Phe Tyr Pro
 20 25 30
 Ser Phe Lys Tyr Met Phe Lys Ile Ile Ile Tyr Val Ser Ala Tyr Cys
 35 40 45
 Arg Thr Ala Leu Arg Ala Thr Val Ser His
 50 55

60

666

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

5
10 Asn Arg Thr Leu Leu Phe Leu Ile Leu Phe Val Leu Phe Gly Leu Gly
1 5 10 15
Tyr Gly Phe

15

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

20
25 Met Phe Leu Leu Val Leu Ser Val Phe Cys Asp Phe Met Cys Ser Ile
1 5 10 15
Ala Pro Arg Cys His Ala Leu Ser Leu Val Ser Leu Arg Ala Gln His
20 25 30
30 Leu Ser Leu Phe Ile Thr Cys His
35 40

35

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

40
45 Met Leu Leu Phe Ile Leu Leu Thr Leu Ser Ser Gly Cys Arg Leu Leu
1 5 10 15
Val Ser Ser Trp Lys Thr Phe Leu Pro His Phe Ser Leu Pro Gly Pro
20 25 30
50 Arg Glu His Pro Glu Gly Ser Arg Thr Trp Phe Phe Arg Tyr Trp Glu
35 40 45
Pro Gly Ala His Cys Leu His Cys Ala
50 55

55

(2) INFORMATION FOR SEQ ID NO: 527:

60

(i) SEQUENCE CHARACTERISTICS:

667

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

5

Ala Arg Leu Leu Leu Phe Leu Ser Ser Val His Pro Ser Ile Met Pro
 1 5 10 15

10

Ser Cys Asn Gln Leu
 20

(2) INFORMATION FOR SEQ ID NO: 528:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Ser Leu Thr Ser Ser Leu Thr Phe Leu Ser His Ile Leu Leu Leu
 1 5 10 15

25

Pro Gln Lys Leu Gln Phe Leu Ser Trp Met Glu Arg Gln Gln Arg Cys
 20 25 30

Thr Gly Val Ala Lys Tyr Ala
 35

30

(2) INFORMATION FOR SEQ ID NO: 529:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Val Leu Arg Leu Ile Gln Leu Ile Phe Leu Ile Phe Phe Ile His
 1 5 10 15

45

Ile Ile Ile Leu Leu Ile Pro Gly Ser Arg Pro Cys Gly Ser Trp Val
 20 25 30

Asn Asp Arg Xaa Leu Gly Leu Arg Asp Val Thr His Leu Ile Tyr Leu
 35 40 45

50

His Trp Val His Gly His Leu Pro Trp Cys His Pro Tyr Ile Gln Val
 50 55 60

Glu Phe Ser Ala Leu Ile Glu Ser Thr Ala Gln Leu Gly Leu Pro Phe
 65 70 75 80

55

Ser Trp Val Arg Val Ile His Pro Phe Leu Val Leu Pro Cys Leu Tyr
 85 90 95

60

Ser Pro Gly Leu Lys Asn Gly Ile Phe Leu Phe Leu Leu Arg Ala Met
 100 105 110

Pro Gly Gly Met Phe Pro Gly Asn Leu Glu Ala Phe Arg Val Pro Val
 115 120 125

5

10 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
 1 5 10 15
 20 Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
 20 25 30
 25 Trp Gly Phe Gly Xaa Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
 35 40 45
 Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
 50 55 60
 30 His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
 65 70 75 80

Pro Asn

35

(2) INFORMATION FOR SEQ ID NO: 531:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15
 50 Tyr Trp Thr Met
 20

55 (2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln Leu Lys Ile
 1 5 10 15
 5 Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu Lys Ile Ile
 20 25 30
 Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser Trp Ala Ile
 35 40 45
 10 Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn Lys Thr Ala
 50 55 60
 Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr
 15 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15
 30 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Xaa Ser Tyr Leu Trp
 20 25 30
 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Xaa Trp Ala Cys
 35 40 45
 35 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu
 50 55 60

40 (2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15
 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30
 55 Ile Leu Phe Phe Ile Val Phe
 35

60 (2) INFORMATION FOR SEQ ID NO: 535:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Leu
1
10

(2) INFORMATION FOR SEQ ID NO: 536:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Asp Gln Phe Lys Ile Phe Tyr Phe Leu Lys Ala Phe Phe Ala Cys
1 5 10 15
25 Cys Asn Val Gln Asp Pro Ser Pro Phe Met Gly Glu Thr Gly Ser Tyr
20 25 30
Leu Asn Ile Gly
35

30

(2) INFORMATION FOR SEQ ID NO: 537:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

40 Met Phe Asp Phe Leu Ser Tyr Phe Lys Asp Leu Leu Ser Cys
1 5 10

45 (2) INFORMATION FOR SEQ ID NO: 538:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Gly Phe Gly Phe Val Leu Asn Ile Phe Ser Phe Phe Leu Xaa Pro
1 5 10 15
55 Pro Leu

60

671

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

5 Leu Leu Leu Trp Thr Leu Leu Ala Xaa Tyr Xaa
 10 1 5 10

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

15 Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 20 1 5 10 15
 25 Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30
 30 Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45
 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60
 35 Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80
 Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
 85 90 95
 40 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

50 Phe Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met
 55 1 5 10 15
 Leu Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr
 20 25 30
 60 Leu Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser
 35 40 45

Pro Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe
 50 55 60

5 Trp Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr
 65 70 75 80

Leu Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val
 85 90 95

10 Asp Gly Glu Glu Leu Gln Met Glu Pro Val
 100 105

15

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

20 Met Asp Arg Phe Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe
 25 1 5 10 15

Phe Asn Ile Gly Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile
 20 25 30

30 Ser Ser Tyr Met Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg
 35 40 45

Tyr Asn Arg Lys Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu
 50 55 60

35 Val Thr Leu Gly Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu
 65 70 75 80

40 Leu Leu Thr Arg Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr
 85 90 95

Ile Ala Pro Thr Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Thr
 100 105 110

45 Gly Cys Ser Ala Ser Ser Thr Leu Pro Phe Arg Trp Ala Val Val Trp
 115 120 125

Ala Thr Leu Gln Ala Pro Lys Xaa
 130 135

50

(2) INFORMATION FOR SEQ ID NO: 543:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

60

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	Met	Ala	Gly	Asp	Trp	His	Trp	Ala	Leu	Arg	Val	Thr	Pro	Gly	Leu	Gly	
	1				5					10					15		
5	Val	Val	Ala	Val	Leu	Leu	Leu	Phe	Leu	Val	Val	Arg	Glu	Pro	Pro	Arg	
				20					25					30			
	Gly	Ala	Val	Glu	Arg	His	Ser	Asp	Leu	Pro	Pro	Leu	Asn	Pro	Thr	Ser	
				35					40					45			
10	Trp	Trp	Ala	Asp	Leu	Arg	Ala	Leu	Ala	Arg	Asn	Pro	Ser	Phe	Val	Leu	
				50				55					60				
	Ser	Ser	Leu	Gly	Phe	Thr	Ala	Val	Ala	Phe	Val	Thr	Gly	Ser	Leu	Ala	
15				65			70				75					80	
	Leu	Trp	Ala	Pro	Ala	Phe	Leu	Leu	Arg	Ser	Arg	Val	Val	Leu	Gly	Glu	
						85				90					95		
20	Thr	Pro	Pro	Cys	Leu	Pro	Gly	Asp	Ser	Cys	Ser	Ser	Ser	Asp	Ser	Leu	
				100					105					110			
	Ile	Phe	Gly	Leu	Ile	Thr	Cys	Leu	Thr	Gly	Val	Leu	Gly	Val	Gly	Leu	
				115				120					125				
25	Gly	Val	Glu	Ile	Ser	Arg	Arg	Xaa	Arg	His	Ser	Asn	Pro	Arg	Ala	Asp	
				130				135					140				
	Pro	Leu	Val	Cys	Ala	Thr	Gly	Leu	Leu	Gly	Ser	Ala	Pro	Phe	Leu	Phe	
30				145			150				155					160	
	Leu	Ser	Leu	Ala	Cys	Ala	Arg	Gly	Ser	Ile	Val	Ala	Thr	Tyr	Ile	Phe	
					165					170					175		
35	Ile	Phe	Ile	Gly	Glu	Thr	Leu	Leu	Ser	Met	Asn	Trp	Ala	Ile	Val	Ala	
				180					185					190			
	Asp	Ile	Leu	Leu	Tyr	Val	Val	Ile	Pro	Thr	Arg	Arg	Ser	Thr	Ala	Glu	
				195				200					205				
40	Ala	Phe	Gln	Ile	Val	Leu	Ser	His	Leu	Leu	Gly	Asp	Ala	Gly	Ser	Pro	
				210				215				220					
	Tyr	Leu	Ile	Gly	Leu	Ile	Ser	Asp	Arg	Leu	Arg	Arg	Asn	Trp	Pro	Pro	
45				225			230				235				240		
	Ser	Phe	Leu	Ser	Glu	Phe	Arg	Ala	Leu	Gln	Phe	Ser	Leu	Met	Leu	Cys	
					245					250				255			
50	Ala	Phe	Val	Gly	Ala	Leu	Gly	Gly	Ala	Leu	Ser	Trp	Ala	Pro	Xaa	Ser	
				260					265					270			
	Ser	Leu	Arg	Pro	Thr	Ala	Gly	Gly	His	Ser	Cys	Thr	Cys	Arg	Ala	Cys	
				275				280					285				
55	Cys	Thr	Lys	Gln	Gly	Pro	Gln	Thr	Thr	Gly	Leu	Trp	Cys	Pro	Ser	Gly	
				290			295					300					
	Ala	Ala	Pro	Pro	Ala	Cys	Pro	Trp	Pro	Val	Cys	Ser	Ser	Glu	Arg	Leu	
60				305		310					315					320	

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Pro Leu Thr Tyr Leu His Ile Cys His Ser Xaa Pro Trp Ala His Pro
 325 330 335

5 Thr Lys Gly Leu Gly Leu Thr Pro Trp Pro Gly Pro Ala Ser Arg Gly
 340 345 350

Thr Leu Gly Arg Val Pro Ala Pro Arg His Tyr Xaa Gly Ser Ser Gly
 355 360 365

10 Glu Glu Val Gly Val Gln Glu Gly Asp Pro Ser Pro Gln Gly Xaa Pro
 370 375 380

Gln Gly Leu Gly Ala Ile Cys Asn Gly Ile Lys Phe Val Ala Arg Pro
 385 390 395 400

15 Gln Val Pro Ala Leu Val Phe Leu Trp Val Ala Ser Asp Leu Ala Pro
 405 410 415

Arg Leu His Pro Arg Ala Pro Glu
 420

20

(2) INFORMATION FOR SEQ ID NO: 544:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Phe Arg Phe Val Ile Cys Leu Phe Leu Trp Leu Val Leu Cys Arg
 1 5 10 15

35 Asp Ser Thr Ser Ala Ser Arg Ile Ala Leu Tyr Tyr Arg Ile Val Phe
 20 25 30

Leu Ile His Gln Cys Ser Ser
 35

40

(2) INFORMATION FOR SEQ ID NO: 545:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Pro Trp Xaa Ala Gln Leu Leu Asp Arg Thr Ile Gly Pro Leu
 1 5 10 15

55 Tyr Leu Leu Phe Val Gln Phe Ser Pro Ala Phe Ser Arg Thr Ser Pro
 20 25 30

Trp Arg Ser Pro Lys Asn Phe Arg Arg Leu Tyr Pro Pro Cys Thr Thr
 35 40 45

60 Ser Gly Cys Ala Ala Arg Trp Leu Phe Ser

50

55

5 (2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Gly Leu Ser Val Leu Leu Pro Leu Cys Leu Leu Gly Pro Gly Arg
 1 5 10 15
 Phe Thr Ser Gly Gln Lys Pro Leu Asp Thr Pro Gly Leu Gly Val Pro
 20 25 30
 Phe

20

25 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
 1 5 10 15
 Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
 20 25 30
 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
 35 40 45
 Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
 50 55 60
 Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
 65 70 75 80
 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala
 85 90 95
 Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr
 100 105 110
 Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln
 115 120 125
 Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala
 130 135 140
 Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu
 145 150 155 160

60

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Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly
 165 170 175
 5 Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu
 180 185 190
 Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val
 195 200 205
 10 Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu
 210 215 220
 Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val
 15 225 230 235 240
 Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys
 245 250 255
 20 Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser
 260 265 270
 Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn
 275 280 285
 25 Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp
 290 295 300
 Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe
 30 305 310 315 320
 Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp
 325 330 335
 35 Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu
 340 345 350
 Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln
 355 360 365
 40

(2) INFORMATION FOR SEQ ID NO: 548:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:
 Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15
 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 55 20 25 30
 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45
 60 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro

677

50 55 60

Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
1 5 10 15
His Cys Trp Gly Leu Pro Leu Ala Cys Gly Thr Phe Val Gln Gly His
20 25 30
Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr
1 5 10 15
Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys
20 25 30
Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys
35 40 45
Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn
50 55 60
Tyr Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile
65 70 75 80
Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala
85 90 95
Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile
100 105 110
Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val
115 120 125
Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg
130 135 140

Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln Ala Lys Leu Pro Gly
 145 150 155 160

5 Ile Ala Lys Lys Lys Ala Glu Xaa
 165

10 (2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Ser Val Pro Phe His Leu Leu Val Val Leu Arg Ser Arg Ala Val Arg
 1 5 10 15
 20 Ala Arg Arg Arg Arg Glu Pro Arg Ser Leu Pro Arg Pro Gly Asp Glu
 20 25 30
 25 Glu Leu Gln Leu Leu Leu Cys Gly Ala Arg Ser Asp Phe Leu Glu Arg
 35 40 45
 Cys Glu Glu Asp Trp Val Cys Leu Trp His His Ala Asp His Ala Ala
 50 55 60
 30 Phe Pro Gly Ser Phe Gln Cys His Gln Cys Gly Phe Leu Pro His Pro
 65 70 75 80
 Gly Ser Ser Leu Cys His His Gln Leu Gln Asp Leu Gln Val Arg His
 85 90 95
 35 Pro Ser Cys Thr Glu Val Arg Arg Arg Pro Ser Ile Gln Ser Leu Pro
 100 105 110
 40 Gly Arg Arg His Tyr Ser Val Leu Arg Ser Phe Pro
 115 120

45 (2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp
 1 5 10 15
 55 Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His
 20 25 30
 Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
 35 40 45
 60

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Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His
 50 55 60

Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu
 5 65 70 75 80

Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro
 85 90 95

Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg
 10 100 105 110

Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr
 115 120 125

Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn
 130 135 140

Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val
 145 150 155 160

Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser
 165 170 175

25 Leu

30 (2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15

Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30

Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45

Thr Glu Gly Ile Pro Cys Ala Lys Ile Pro Glu Trp Val Thr His Leu
 50 55 60

Thr Trp Gln Thr Leu Lys Asn Ser
 65 70

55 (2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Val Leu Arg Ile Ile Cys Leu Trp Pro Cys Gly Thr Thr Leu Pro Leu
 1 5 10 15
 Val Glu Lys Ala His Asp Ser His Ser Ala Asp Pro Val Cys Pro Gly
 20 25 30
 10 Leu Thr Ala His Leu Pro Val Leu Leu Tyr Val Gln Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Lys His Ala Asp Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser
 1 5 10 15
 25 Pro Leu Leu Met Thr Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu
 20 25 30
 Ser Leu Gly Pro Arg Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg
 35 40 45
 30 Gly Phe Met Ile Val Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr
 50 55 60
 Ile Val Tyr Glu Phe Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp
 35 65 70 75 80
 Arg Cys Asp Pro Gln Asp Cys Thr Leu Gly Gln Cys Pro Ser Val Pro
 85 90 95
 40 Ser Pro Xaa Thr Pro Val Thr Lys Ala Tyr Val Val Arg Thr Glu Gln
 100 105 110
 Gly Thr Gly Pro Pro Leu Pro Thr Ala Ala Leu Gln Gly Pro Arg Leu
 115 120 125
 45 Trp Phe Leu Thr His Phe Pro Arg Ala Ala Pro Gly Met Trp Pro His
 130 135 140
 Cys Cys Leu Pro Leu Gln Ser Trp Gly Leu Lys Gly Leu Tyr Ser Tyr
 50 145 150 155 160
 Phe Pro Leu Pro Ala Leu Lys Leu Gly Arg Gly Ala Leu Arg Ala Gly
 165 170 175
 55 Pro Thr Lys Gly Leu Val Ala Phe Phe Leu Thr Gln Lys Arg Ser Ala
 180 185 190
 Ile Met Ser Leu Trp Thr Gln Ser His Ser Ser Thr Pro His Thr Glu
 195 200 205
 60

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Ala Val Ala Ser Gly Pro Lys Val Arg Val Gly Gly Gly Leu Gly Ile
 210 215 220

5 Gln Pro Val Glu Ala Ala Tyr Ser Thr Cys Val Leu Ile Lys Ser Asp
 225 230 235 240

Arg Gly Asn His Glu Lys Lys Lys Lys Lys Lys
 245 250

10

(2) INFORMATION FOR SEQ ID NO: 556:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Gly Leu Ala Gly Leu Cys Gly Gln Leu Ser Ser Pro Ala Leu Cys Val
 1 5 10 15

Asn Arg Leu

25

(2) INFORMATION FOR SEQ ID NO: 557:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

35 Met Ile Thr Glu Lys Trp Gly Leu Asn Met Glu Tyr Cys Arg Gly Gln
 1 5 10 15

40 Ala Tyr Ile Xaa Ser Ser Gly Phe Ser Ser Lys Met Lys Val Val Ala
 20 25 30

Ser Arg Leu Leu Glu Lys Tyr Pro Gln Ala Ile Tyr Thr Leu Cys Ser
 35 40 45

45 Ser Cys Ala Leu Asn Met Trp Leu Ala Lys Ser Val Pro Val Met Gly
 50 55 60

Val Ser Val Ala Leu Gly Thr Ile Glu Glu Val Cys Ser Phe Phe His
 65 70 75 80

50 Arg Ser Pro Gln Leu Leu Leu Glu Leu Asp Asn Val Ile Ser Val Leu
 85 90 95

55 Phe Gln Asn Ser Lys Glu Arg Gly Lys Glu Leu Lys Glu Ile Cys His
 100 105 110

Ser Gln Trp Thr Gly Arg His Asp Ala Phe Glu Ile Leu Val Glu Leu
 115 120 125

60 Leu Gln Ala Leu Val Leu Cys Leu Asp Gly Ile Asn Ser Asp Thr Asn

682

130 135 140

Ile Arg Trp Asn Asn Tyr Ile Ala Gly Arg Ala Phe Val Leu Cys Ser
 145 150 155 160

5 Ala Val Ser Asp Phe Asp Phe Ile Val Thr Ile Val Val Leu Lys Asn
 165 170 175

10 Val Leu Ser Phe Thr Arg Ala Phe Gly Lys Asn Leu Gln Gly Gln Thr
 180 185 190

 Ser Asp Val Phe Phe Ala Ala Gly Ser Leu Thr Ala Val Leu His Ser
 195 200 205

15 Leu Asn Glu Val Ile Gly Lys Tyr Xaa
 210 215

20 (2) INFORMATION FOR SEQ ID NO: 558:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 82 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu Asn Glu
 1 5 10 15

30 Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg Asn Thr
 20 25 30

Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile Asn Phe
 35 35 40 45

Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile Lys Leu
 50 55 60

40 Tyr Thr Ser Lys Ser Glu Leu Pro Thr Asp Asn Ser Glu Thr Val Glu
 65 70 75 80

Asn Thr

45

(2) INFORMATION FOR SEQ ID NO: 559:

50

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 95 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

55

Met Val Leu Ile Leu Leu Asn Leu Leu Leu Gly Gln Phe Ser Cys Met
 1 5 10 15

60

Ser Pro Ala Ser His His Cys His Pro Leu Pro Thr Glu Met Pro Cys
 20 25 30

Ser Ser Asp Trp Gly Phe Asp Ser His Thr Val Tyr Pro Ser Cys Val
 35 40 45

5 Asp Ala Leu Leu Pro Lys Pro Ser Ala Asn Ser Phe Pro Asn Gly Ser
 50 55 60

Cys His Cys Gln Gly Leu Tyr Asn Gln Gln Gln Gln Asn Leu His Ala
 65 70 75 80

10 Ala Glu Gly Pro Ala Ser Leu Arg Cys Asn Lys Tyr Val Ser Thr
 85 90 95

15

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

25 Met Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile
 1 5 10 15

Val Phe Thr Val Ile Gly Asp Ala Pro Gly Ala Val Leu Ser Cys Ala
 20 25 30

30 Gly His Pro Cys Val Gly Phe Ala Ala Val Leu Val Ala Pro Leu Thr
 35 40 45

Val Ala Val Ser Ser Xaa
 50

35

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

45

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 1 5 10 15

50 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro
 35 40 45

55 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys
 50 55 60

Asp Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu
 65 70 75 80

60

684

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg Ile
85 90 95

5 Asn Val Gly Leu Arg Gly Trp Trp Leu Val Ala Xaa
100 105

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
1 5 10 15

20 Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
20 25 30

Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
35 40 45

25 Ala Pro
50

30

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
20 25 30

45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
50 55 60

50 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
65 70 75 80

55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
100 105 110

60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

685

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg
145 150 155 160

10 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Thr
165 170 175

Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
180 185 190

15 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
195 200 205

Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
210 215 220

20 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
225 230 235 240

25 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn Xaa
245 250

30 (2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Ser Phe Leu Met Trp Leu Met Ser Leu Ala Ile Thr Ser Gln Pro
1 5 10 15

40 Pro Met

45 (2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
1 5 10 15

55 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
20 25 30

60 Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
35 40 45

686

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

5 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Phe
 65 70 75 80

10

(2) INFORMATION FOR SEQ ID NO: 566:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

20

His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln Val Leu Ser
 1 5 10 15

25

Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu Ala Pro Gly Arg
 20 25 30

Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro Trp Phe Thr Ala
 35 40 45

30

Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys Arg Gln Arg Arg
 50 55 60

Gln Glu Arg Arg Gln Met Lys Arg Leu
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 567:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

45

Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys Lys Glu Glu Val Ile
 1 5 10 15

50

Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser
 20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
 35 40 45

55

Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
 50 55 60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
 65 70 75 80

60

687

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
 85 90 95
 5 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
 100 105 110
 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
 115 120 125
 10 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
 130 135 140
 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
 15 145 150 155 160
 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
 165 170 175
 20 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
 180 185 190
 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro
 195 200 205
 25 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
 210 215 220
 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
 30 225 230 235 240
 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
 245 250 255
 35 Asp Ser Gly Asp Glu Ala Xaa
 260

40 (2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Met Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala
 1 5 10 15
 50 Leu Arg Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Leu
 20 25 30
 Leu Phe Gly Leu Thr His Leu Asn Pro Ser Ala Lys Leu Leu Leu Ser
 35 40 45
 55 Gln Met Lys Thr Ser Gly Asn Arg Lys Ser Glu Tyr Ser Lys Tyr Ala
 50 55 60
 60 Arg Asn Trp Lys Lys His
 65 70

(2) INFORMATION FOR SEQ ID NO: 569:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Pro Val Thr Ser Lys Arg Thr Leu Phe Phe Pro Asp Pro Cys Ser
 1 5 10 15
 Tyr Asp Thr Pro Pro Asp Cys His Cys His Ser Phe Arg Ala Glu
 20 25 30

Leu Leu

20

(2) INFORMATION FOR SEQ ID NO: 570:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 1 5 10 15
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 20 25 30
 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 35 40 45
 His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ser
 50 55 60
 Lys Ala Pro Asn Ser Leu Gly Thr Thr Gly Leu Trp Ser Thr Val Tyr
 65 70 75 80
 Ile Phe Thr Glu Val Phe His Asn Phe Ser Asn Asn Ser Ile Phe Ser
 85 90 95
 Gly Lys Phe Leu Tyr Glu Val Xaa
 100

50

(2) INFORMATION FOR SEQ ID NO: 571:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

689

Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu Leu His Ile Val Leu
 1 5 10 15

5 Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala Trp Thr Leu Thr Asn
 20 25 30

Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu His Ala Val Lys Gly
 35 40 45

10 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
 50 55 60

15 Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr Ser Ser Arg Lys Phe
 65 70 75 80

Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu Ala Ser Phe Tyr Thr
 85 90 95

20 Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr Ala Ser Leu Leu Ser
 100 105 110

Val Leu Ile Pro Lys Met Pro Gln Leu His Gly Val Arg Ile Phe Gly
 115 120 125

25 Ile Asn Lys Tyr
 130

30

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

40 Met Asn Lys Trp Ile Cys Glu Met His Cys Tyr Leu Val Leu Leu Ser
 1 5 10 15

Val Cys Ser Pro Ser Ala Leu Arg Arg Val Arg His Thr Leu Ser Arg
 20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

55 Met Pro Val Leu Ser Leu Leu Cys Thr Leu Ile Val Ser Phe Gln Ser
 1 5 10 15

60

690

Ala Asp Ser Cys Glu Val Phe Leu Asn Cys Ser Leu
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

15

Met Lys Val Ser Thr Met Leu Trp Phe Leu Cys Trp Glu Gln Ser His
 1 5 10 15

Phe Leu Arg Glu Trp Glu Asp Leu Ser Thr Phe Leu Ile Leu Ile Gln
 20 25 30

20

Met Glu Cys Gln Tyr Gly Asn Ser
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

35

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser
 1 5 10 15

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Xaa Leu
 20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

50

Met Lys Arg Gly Cys Leu Gly Leu Leu Phe Phe Ser Cys Cys Ser Ser
 1 5 10 15

Ala Pro Thr Met Leu Leu Cys Asp Tyr Leu Asn Trp Phe
 20 25

55

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

60

691

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

5 Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val
 1 5 10 15

Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu
 20 25 30

10 Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys
 35 40 45

Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys
 15 50 55 60

Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Xaa Asn Arg Arg Arg
 65 70 75 80

20 Xaa Val Arg Gly Leu Pro Ser Xaa Leu Thr Asn Ser
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15

35 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30

Arg Val Met Val Asn Leu Asn Ile Leu Phe
 40 35 40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 1 5 10 15

55 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Pro Pro Leu Ser
 20 25 30

Thr Phe Thr Ser Asp Phe Tyr Phe Met Glu Phe Gly Ile Glu Val Lys
 35 40 45

60

Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr Lys
 50 55 60

5 Lys Phe Asn Lys Lys Lys
 65 70

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Leu Arg Leu Leu Leu Val Ala Phe Ala Leu Val Val Val Leu
 1 5 10 15

20 Phe His Val Leu Leu Ala Pro Ile Thr Ala Leu Phe His Thr His Phe
 20 25 30

Tyr Asp Arg Leu Gln Asp Ala Gly Ser Arg Trp Pro Glu Leu Tyr Leu
 35 40 45

25 Tyr Ser Arg Ala Asp Glu Val Val Leu Ala Arg Asp Ile Glu Arg Met
 50 55 60

30 Val Glu Ala Arg Leu Ala Arg Arg Val Leu Ala Arg Ser Val Asp Phe
 65 70 75 80

Val Ser Ser Ala His Val Ser His Leu Arg Asp Tyr Pro Thr Tyr Tyr
 85 90 95

35 Thr Ser Leu Cys Val Asp Phe Met Arg Asn Cys Val Arg Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Met Phe Lys Leu Glu Glu Cys Gly Lys Thr Thr Phe Leu Leu Ser Met
 1 5 10 15

50 Ala Leu Tyr Phe Trp Trp Ile Val Gln Thr Thr Lys Gly Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

5 Met Glu Ser Asp Ala Leu Leu Leu Thr Ile Phe Trp Ile Ile Ala Arg
 1 5 10 15
 Ser Ser Val Arg Ser Val Gly Lys Ser Ser Gln Arg Ser Phe Thr Thr
 20 25 30
 10 Ile Thr Gln Leu Arg Ser Thr His Thr Gly Pro Ser Arg Arg Ser Tyr
 35 40 45
 Leu Ile Trp Trp Asn Gly Gly Pro Lys Arg Thr Ile Ser Tyr Val Ser
 50 55 60
 15 Arg Arg Phe Arg Ser Phe Arg
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

30 Val Gly Leu Phe Gln Pro Lys Thr Phe Gln Val Pro Val Thr Asp Leu
 1 5 10 15
 Tyr Ile Phe Ile Lys Ile Tyr Ser Glu Ile Gly Pro Ile Met His Val
 20 25 30
 35 Leu Cys Pro Gly Tyr Ser Gln Ser Pro Ser Thr Pro Pro Trp Thr
 35 40 45

40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

50 Met Trp Phe Gly Ser Asp Arg Ser Asp Leu Arg Ile Gly Thr Ala Phe
 1 5 10 15
 Leu Phe Asp Leu Val Cys Asp Leu Cys Ile His Ala Trp Lys Pro Pro
 20 25 30
 55 Gly Leu Val Arg Phe Ser Phe
 35

60

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Leu Asn Thr Ala Ser Leu Asn Leu Pro Trp Lys Val Gln Leu Phe
 1 5 10 15

10 Ala His Ala

15 (2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Ala Cys Leu Leu Leu Phe Leu Ala Phe Ser Trp Lys Arg Lys
 1 5 10 15

25 Gly Leu Trp Ser Gly Pro Gly
 20

30

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

40 Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15

Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30

45 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45

Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60

50

Ala His Thr Val Ala
 65

55

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

60

695

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

5 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
 1 5 10 15
 Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
 20 25 30
 10 Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu
 35 40 45
 Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
 50 55 60
 15 Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys
 65 70 75

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

30 Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15
 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30
 35 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45
 Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60
 40 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
 65 70 75 80
 45 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95
 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110
 50 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 115 120 125
 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140
 55 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 145 150 155

60

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

5 Met Pro Glu Thr Arg Leu Gly His Arg Gln Gln Phe Ala Val Phe His
 10 1 5 10 15
 Leu Xaa Pro Val Pro Pro Cys Gly
 20

15

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

20 Met Leu Thr Phe Leu Phe Ser Ala Cys Ala Thr Cys Leu Gly Lys Leu
 25 1 5 10 15
 Ala Ser Pro Leu Ala Pro Val Gly Pro Gln Gln Arg Gly Xaa Pro Pro
 30 20 25 30
 Gly Pro Pro Leu Leu Ser
 35

35

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

40 Met Asp Pro Phe His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu
 45 1 5 10 15
 Val Phe Ala Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser
 20 25 30
 Arg Arg Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp
 50 35 40 45
 Glu Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
 55 50 55 60
 Gln Lys Ala Glu Asn
 65

60

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

5 Asn Leu Arg Val Arg Leu Gly Asp Val Ile Ser Ile Gln Pro Cys Pro
 1 5 10 15
 Asp Val Lys Tyr Gly Lys Arg Ile His Val Leu Pro Ile Asp Asp Thr
 20 25 30
 15 Val Glu Gly Ile Thr Gly Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr
 35 40 45
 Phe Leu Glu Ala Tyr Arg Pro Ile Arg Lys Gly Asp Ile Phe Leu Val
 50 55 60
 20 Arg Gly Gly Met Arg Ala Val Glu Phe Lys Val Val Glu Thr Asp Pro
 65 70 75 80
 25 Ser Pro Tyr Cys Ile Val Ala Pro Asp Thr Val Ile His Cys Glu Gly
 85 90 95
 Glu Pro Ile Lys Arg Glu Asp Glu Glu Glu Ser Leu Asn Glu Val Gly
 100 105 110
 30 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu
 115 120 125
 Met Val Glu Leu Pro Leu Arg His Pro Ala Leu Phe Lys Ala Ile Gly
 130 135 140
 35 Val Lys Pro Pro Arg Gly Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly
 145 150 155 160
 40 Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe
 165 170 175
 Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser
 180 185 190
 45 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro
 195 200 205
 Ala Ile Ile Phe Ile Asp Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu
 210 215 220
 50 Lys Thr His Gly Glu Val Glu Arg Arg Ile Val Ser Gln Leu Leu Thr
 225 230 235 240
 55 Leu Met Asp Gly Leu Lys Gln Arg Ala His Val Ile Val Met Ala Ala
 245 250 255
 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
 260 265 270
 60 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu

698

275 280 285

Glu Ile Leu Gln Ile His Thr Lys Asn Met Lys Leu Ala Asp Asp Val
 290 295 300

5 Asp Leu Glu Gln
 305

10

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

20 Met Gln Ile Lys Leu Leu Lys Ser Val Lys Thr Val Phe Ala Ile Thr
 1 5 10 15

Leu Leu Val Leu Phe Leu
 20

25

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

35 Met Phe Pro Lys Phe Cys Pro Ile Leu Ser Leu Val Asp Phe Ile Ser
 1 5 10 15

His Arg Asp Lys Pro Glu Thr Glu
 20

40

(2) INFORMATION FOR SEQ ID NO: 596:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

50

Met Leu Ile Glu Cys Ala Trp Gln Leu Met Phe Leu Leu Leu Lys Val
 1 5 10 15

55 Glu Gln Leu Gly Ile Leu Asp Lys
 20

60

(2) INFORMATION FOR SEQ ID NO: 597:

699

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:
- Met
 1
- 10
- (2) INFORMATION FOR SEQ ID NO: 598:
- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:
- 20 Met Cys Ile Met Ser Ala Leu Val
 1 5
- 25 (2) INFORMATION FOR SEQ ID NO: 599:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:
- Met Phe Leu Val Trp Phe Phe Trp Gly Leu Ile Ser Ala Leu Ser Asn
 1 5 10 15
- 35 Val His Thr Pro Ser Arg Leu Pro Ala
 20 25
- 40
- (2) INFORMATION FOR SEQ ID NO: 600:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:
- Met Xaa Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
 1 5 10 15
- 50 Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25
- 55
- (2) INFORMATION FOR SEQ ID NO: 601:
- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids

700

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

5 Met Trp Thr Arg Ser Ser Arg Cys Leu Leu Leu Cys Ile Pro Gly Xaa
 1 5 10 15

Ser Arg Arg Arg Arg Ala Gly Ser Gly Met Lys Pro Arg Ser Trp Ser
 20 25 30

10 Ala Trp Arg Pro Ser Gly Gly Thr Gly Thr Ser Ser Ser Gln Ser Ser
 35 40 45

15 Thr Gln Ser Arg Thr Leu Ser Ala Thr Ala Ser Pro Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
 1 5 10 15

30 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

Met Pro Pro Lys Gln Glu Leu Gly Ser Gly Val Gly Glu Leu Ala Lys
 1 5 10 15

45 Asn Ser Lys Arg Gln His Trp Asn His Arg Trp Lys Lys Tyr Leu Lys
 20 25 30

50 Leu Ile Arg Trp Glu Asp Gly Leu Leu Leu Glu Gly Leu Leu Leu Val
 35 40 45

Leu Glu His Cys Ala Thr Met Ala Trp Asp Cys Leu Met Arg Leu Glu
 50 55 60

55 Leu Leu Lys Arg Leu
 65

60

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Lys Ile Val Tyr Ile Leu Gly Asn Pro Leu Lys Phe Asn Ser Arg Val
 1 5 10 15
 Ile His His Leu Val Leu Leu Gln
 20

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Met Asn Leu His Gln Arg Arg Leu Leu Leu Ile Gly His Leu Met Thr
 1 5 10 15
 Leu Val Lys Ala Ser Lys Ser Phe Ser Phe Thr Glu Ile Thr Ser Ser
 20 25 30
 Arg Lys Lys
 35

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr
 1 5 10 15
 Tyr Asn Ile His Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val
 20 25 30
 Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr
 35 40 45
 Val Gly Pro Thr Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu
 50 55 60
 His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Xaa
 65 70 75 80
 Glu Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln
 85 90 95

Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro
 100 105 110
 5 Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln
 115 120 125
 Ser His
 130

10

(2) INFORMATION FOR SEQ ID NO: 607:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

20 Met Leu Val Ile Phe Leu Phe Thr Ser Leu Leu Lys Ile Pro Ser Ser
 1 5 10 15
 Val Pro Gly Leu Ile Asn Val
 20

25

(2) INFORMATION FOR SEQ ID NO: 608:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

35

Glu Leu Asp Tyr Ile Leu
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 609:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

50 Met Ala Pro Pro Gly Trp Gln Xaa Xaa Xaa Xaa Xaa Trp Leu Ala Cys
 1 5 10 15
 Pro Asp Arg Gly Glu Leu Ser Ser Arg Ser Pro Pro Cys Arg Leu Ala
 20 25 30
 55 Arg Trp Ala Glu Gly Asp Arg Glu Thr Arg Thr Cys Leu Leu Glu Leu
 35 40 45
 Ser Ala Gln Ser Trp Gly Gly Arg Phe Arg Arg Ser Ser Ala Val Ser
 50 55 60

60

703

Ala Gly Ser Pro Ser Arg Leu His Phe Leu Pro Gln Pro Leu Leu Leu
 65 70 75 80

5 Arg Ser Ser Gly Ile Pro Ala Ala Ala Thr Pro Trp Pro Gln Pro Ala
 85 90 95

Gly Leu Pro Val Arg Pro Thr Pro Thr Arg Thr Gly Glu Glu Asp Arg
 100 105 110

10 Thr Leu Asp Ile Ser Ile Cys Thr Glu Val Leu Ala Gly Thr Glu Gln
 115 120 125

Pro Pro Pro Pro Arg Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg
 130 135 140

15 Leu Glu Thr Leu Asp Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg
 145 150 155 160

20 Gly Lys Leu Asp Phe Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe
 165 170 175

Gln Gly Glu Asp Arg Lys Phe Ala Pro Ser Asp Lys Ser Gln Pro Pro
 180 185 190

25 Thr Thr Glu Arg Glu Gln Val Pro Val Ser Arg Ile Gln Thr Asp Leu
 195 200 205

Thr Glu Ile Gly Ser Ser Met Arg Ser Pro Gly Val Ser Pro Arg Ile
 210 215 220

30 Trp Leu Asp Phe Gln Ser Thr Xaa
 225 230

35

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

45 Met Val Leu Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu
 1 5 10 15

Leu Leu Asn Met Leu Ile Ala Leu Met Xaa Arg Asp Arg Gln Gln Cys
 20 25 30

50 Arg His

55

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Met Val Phe Glu Gly Phe Ser Ser Ala Phe Cys Leu Ser Ser Thr Ala
 1 5 10 15
 5 Pro Thr Ser His Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

Gly Lys Lys Asn Gln Leu Leu Val Ile
 1 5
 20

(2) INFORMATION FOR SEQ ID NO: 613:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 1 5 10 15

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys
 20 25
 35

(2) INFORMATION FOR SEQ ID NO: 614:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

Met Ala Lys Arg Ser Pro Gly Gly Cys Gly Ser Gly Leu Ile Leu Leu
 1 5 10 15

50

Cys Cys Gln Pro Cys Arg Pro Thr Ser Ser Ala Pro Met Arg
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

5	Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Xaa Glu Tyr	1	5	10	15
	Pro Thr Phe Val Arg Asn Xaa Gly Val Met Val Cys Ser Ser Leu Cys	20	25	30	
10	Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg Glu	35	40	45	
	Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu Leu	50	55	60	
15	Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala Leu	65	70	75	80
	Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro	85	90	95	
20	Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser Gly	100	105	110	
25	Thr				

30 (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu
1 5 10 15
Asn Thr

45 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

Pro Arg Val Arg Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly
55 1 5 10 15

Asp Ser Cys Lys Leu
 20

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

10 Gln Ala Asp Asp Leu Gln Ala Thr Val Ala Ala Leu Cys Val Leu Arg
 1 5 10 15

Gly Gly Gly Pro Trp Ala Gly Ser Trp Leu Ser Pro Lys Thr Pro Gly
 20 25 30

15 Ala Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg
 35 40 45

20 Lys Arg Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO: 619:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu Ala Xaa Xaa
 1 5 10 15

35 Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp Phe Gly Gly
 20 25 30

Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu
 35 40 45

40 Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val Val Pro Gly
 50 55 60

45 Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val Met Gly Val
 65 70 75 80

Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys Leu Glu Phe
 85 90 95

50 Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Ile Gln Tyr
 100 105 110

Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln Glu Ala Trp
 115 120 125

55 Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala Ala Arg Xaa
 130 135 140

60 His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg Gln Val Arg
 145 150 155 160

[illegible]

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly
 1 5 10 15
 30 Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser
 20 25 30
 Gly Ala Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 621:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15
 50 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30
 Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 55 His Lys Ala Lys Ser His Pro Glu Val
 50 55

60 (2) INFORMATION FOR SEQ ID NO: 622:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:
- Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln
1 5 10 15
Pro Ser Asp
- (2) INFORMATION FOR SEQ ID NO: 623:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:
- Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser
1 5 10 15
Lys Ser Tyr
- (2) INFORMATION FOR SEQ ID NO: 624:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:
- Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys Ile Phe
1 5 10 15
Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met Asn Ser
20 25 30
Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser Asp Ser
35 40 45
Ala Gly Pro
50
- (2) INFORMATION FOR SEQ ID NO: 625:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala
 1 5 10 15
 5 His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys
 20 25 30
 Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu
 35 40 45
 10 Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

20

25 Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser
 1 5 10 15
 Ser His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

35

40 Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser
 1 5 10 15
 Glu Pro Asn Thr Asp Gln Leu Asp Tyr
 20 25

45

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

50

55

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15
 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30

60

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 5 His Lys Ala Lys Ser His Pro Glu Val Xaa Ile Thr Ser Thr Asp Ile
 50 55 60
 Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln Pro Ser Asp Xaa Asn Ser
 65 70 75 80
 10 Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys Ser
 85 90 95
 Tyr Xaa Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys
 15 100 105 110
 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
 115 120 125
 20 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
 130 135 140
 Asp Ser Ala Gly Pro Xaa Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala
 145 150 155 160
 25 Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His
 165 170 175
 Thr Gly Glu Lys His Tyr Xaa
 30 180

35 (2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His
 1 5 10 15
 45 Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys
 20 25 30
 Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln
 35 40 45
 50 Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp
 50 55 60

55 (2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

60 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu
5 1 5 10 15

Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

20	Glu Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu	
	1 5 10 15	
	Met Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val	
	20 25 30	
25	Leu Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu	
	35 40 45	
	Trp Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg	
	50 55 60	
30	Met Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val	
	65 70 75 80	
	Gln Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu	
	85 90 95	
	Asn Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met	
	100 105 110	
40		

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

50 Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg Pro Thr Gly Gln Gln
1 5 10 15
55 Leu Glu Ser Leu Gly Leu Leu Ala
20

60 (2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

Val His Arg Glu Glu Ala Ser Cys Tyr Cys Gln Ala Glu Pro Ser Gly
 1 5 10 15

10 Asp Leu

15 (2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Arg Pro Ala Leu Arg Gln Ala Gly Gly Gly Thr Arg Glu Pro Arg Gln
 1 5 10 15

25

Lys Arg Trp Ala Gly Leu
 20

30

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

Ala Val Asn Phe Arg Pro Gln Arg Ser Gln Ser Met
 1 5 10

40

45 (2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val
 1 5 10 15

Ser Leu Phe Leu Val Val Leu Tyr His Tyr Val Ala Val Asn Asn
 20 25 30

Pro Lys Lys Gln Glu
 35

60

(2) INFORMATION FOR SEQ ID NO: 637:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

10

Glu Glu Met Ala Asp Ser Val Lys Thr Phe Leu Gln Asp Leu Ala Arg
1 5 10 15

15

Gly Ile Lys Asp Ser Ile Trp Gly Ile Cys Thr Ile Ser Lys Leu Asp
20 25 30

Ala Arg Ile Gln Gln Lys Arg Glu Glu Gln Arg Arg Arg Arg Ala Ser
35 40 45

20

Ser Val Leu Ala Gln Arg Arg Ala Gln Ser Ile Glu Arg Lys Gln Glu
50 55 60

Ser Glu Pro Arg Ile Val Ser Arg Ile Phe Gln Cys Cys Ala Trp Asn
65 70 75 80

25

Gly Gly Val Phe Trp Phe Ser Leu Leu Leu Phe Tyr Arg Val Phe Ile
85 90 95

30

Pro Val Leu Gln Ser Val Thr Ala Arg Ile Ile Gly Asp Pro Ser Leu
100 105 110

His Gly Asp Val Trp Ser Trp Leu Glu Phe Phe Leu Thr Ser Ile Phe
115 120 125

35

Ser Ala Leu Trp Val Leu Pro Leu Phe Val Leu Ser Lys Val Val Asn
130 135 140

Ala Ile Trp Phe Gln Asp Ile Ala Asp Leu Ala Phe Glu Val Ser Gly
145 150 155 160

40

Arg Lys Pro His Pro Phe Pro Ser Val Ser Lys Ile Ile Ala Asp Met
165 170 175

Leu Phe Asn Leu Leu Leu Gln Ala Leu Phe Leu Ile Gln Gly Met Phe
180 185 190

45

Val Ser Leu Phe Pro Ile His Leu Val Gly Gln Leu Val Ser Leu Leu
195 200 205

50

His Met Ser Leu Leu Tyr Ser Leu Tyr Cys Phe Glu Tyr Arg Trp Phe
210 215 220

Asn Lys Gly Ile Glu Met His Gln Arg Leu Ser Asn Ile Glu Arg Asn
225 230 235 240

55

Trp Pro Tyr Tyr Phe Gly Phe Gly Leu Pro Leu Ala Phe Leu Thr Ala
245 250 255

Met Gln Ser Ser Tyr Ile Ile Ser Gly Cys Leu Phe Ser Ile Leu Phe
260 265 270

60

Pro Leu Phe Ile Ile Ser Ala Asn Glu Ala Lys Thr Pro Gly Lys Ala
 275 280 285

5 Tyr Leu Phe Gln Leu Arg Leu Phe Ser Leu Val Val Phe Leu Ser Asn
 290 295 300

Arg Leu Phe His Lys Thr Val Tyr Leu Gln Ser Ala Leu Ser Ser Ser
 305 310 315 320

10 Thr Ser Ala Glu Lys Phe Pro Ser Pro His Pro Ser Pro Ala Lys Leu
 325 330 335

Lys Ala Thr Ala Gly His
 340

15

20 (2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Met Ala Lys Phe Met Thr Pro Val Ile Gln Asp Asn Pro Ser Gly Trp
 1 5 10 15

30 Gly Pro Cys Ala Val Pro Glu Gln Phe Arg Asp Met Pro Tyr Gln Pro
 20 25 30

Phe Ser Lys Gly Asp Arg Leu Gly Lys Val Ala Asp Trp Thr Gly Ala
 35 40 45

Thr Tyr Gln Asp Lys Arg Tyr Thr Asn Lys Tyr Ser Ser Gln Phe Gly
 50 55 60

40 Gly Gly Ser Gln Tyr Ala Tyr Phe His Glu Glu Asp Glu Ser Ser Phe
 65 70 75 80

Gln Leu Val Asp Thr Ala Arg Thr Gln Lys Thr Ala Tyr Gln Arg Asn
 85 90 95

45 Arg Met Arg Phe Ala Gln Arg Asn Leu Arg Arg Asp Lys Asp Arg Arg
 100 105 110

Asn Met Leu Gln Phe Asn Leu Gln Ile Leu Pro Lys Ser Ala Lys Gln
 115 120 125

50 Lys Glu Arg Glu Arg Ile Arg Leu Gln Lys Lys Phe Gln Lys Gln Phe
 130 135 140

Gly Val Arg Gln Lys Trp Asp Gln Lys Ser Gln Lys Pro Arg Asp Ser
 145 150 155 160

Ser Val Glu Val Arg Ser Asp Trp Glu Val Lys Glu Glu Met Asp Phe
 165 170 175

60 Pro Gln Leu Met Lys Met Arg Tyr Leu Glu Val Ser Glu Pro Gln Asp

	180	185	190
5	Ile Glu Cys Cys Gly Ala Leu Glu Tyr Tyr Asp Lys Ala Phe Asp Arg 195 200 205		
	Ile Thr Thr Arg Ser Glu Lys Pro Leu Arg Xaa Xaa Lys Arg Ile Phe 210 215 220		
10	His Thr Val Thr Thr Thr Asp Asp Pro Val Ile Arg Lys Leu Ala Lys 225 230 235 240		
	Thr Gln Gly Asn Val Phe Ala Thr Asp Ala Ile Leu Ala Thr Leu Met 245 250 255		
15	Ser Cys Thr Arg Ser Val Tyr Ser Trp Asp Ile Val Val Gln Arg Val 260 265 270		
	Gly Ser Lys Leu Phe Phe Asp Lys Arg Asp Asn Ser Asp Phe Asp Leu 275 280 285		
20	Leu Thr Val Ser Glu Thr Ala Asn Glu Pro Pro Gln Asp Glu Gly Asn 290 295 300		
25	Ser Phe Asn Ser Pro Arg Asn Leu Ala Met Glu Ala Thr Tyr Ile Asn 305 310 315 320		
	His Asn Phe Ser Gln Gln Cys Leu Arg Met Gly Lys Glu Arg Tyr Asn 325 330 335		
30	Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met Asp Lys Asn Glu 340 345 350		
	Ile Ala Ser Val Ala Tyr Arg Tyr Arg Ser Gly Lys Leu Gly Asp Asp 355 360 365		
35	Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val Met Thr Gly Ala 370 375 380		
40	Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu Asn Glu Trp Asp 385 390 395 400		
	Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys Leu Asp Ser Gln 405 410 415		
45	Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn Ser Tyr Lys Leu 420 425 430		
	Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser Glu Tyr Leu Lys 435 440 445		
50	Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser Ser Arg His Val 450 455 460		
55	Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe Ala Ser Gln Ile 465 470 475 480		
	Asn Leu Ser Val Glu Asn Ala Trp Gly Ile Leu Arg Cys Val Ile Asp 485 490 495		
60	Ile Cys Met Lys Leu Glu Glu Gly Lys Tyr Leu Ile Leu Lys Asp Pro		

500 505 510

Asn Lys Gln Val Ile Arg Val Tyr Ser Leu Pro Asp Gly Thr Phe Ser
515 520 525

5 Ser

10

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

20 Lys Lys Arg His Thr Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile
1 5 10 15

Thr Thr Asp Leu Gly Lys His Gln His Met His Asp Arg Asp Asp Leu
20 25 30

25 Tyr Ala Glu Gln Met Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala
35 40 45

Phe Lys Asn Phe Ile Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu
50 55 60

30 Glu Phe Glu Val Pro Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr
65 70 75 80

35 Arg Ser Thr Cys Leu Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala
85 90 95

Thr Glu Trp Pro Pro Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile
100 105 110

40 His Phe Xaa Arg Val Gln Phe His Leu Lys Asn Phe Asp Met Val Ile
115 120 125

Val Tyr Lys Asp Tyr Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro
130 135 140

45 Val Ala Ser Leu Asp Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu
145 150 155 160

50 Lys Tyr Thr Glu Gly Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys
165 170 175

Thr Ile Val Asp Asp Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser
180 185 190

55 Phe Leu

60 (2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Arg Ser Gly Leu Gly Leu Gly Ile Thr Ile Ala Phe Leu Ala Thr Leu
 1 5 10 15
 Ile Thr Gln Phe Leu Val Tyr Asn Gly Val Tyr Gln Tyr Thr Ser Pro
 20 25 30
 Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly
 35 40 45
 Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro
 50 55 60
 Glu Lys Pro His Ser Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser Val Glu
 1 5 10 15
 Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Xaa Xaa Pro Xaa
 20 25 30
 Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr
 35 40 45
 Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe
 50 55 60
 Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile Ser Asn
 65 70 75 80
 Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp
 85 90 95
 Thr Arg Arg Ser Gly
 100

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

5 Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln Leu
 1 5 10 15
 Gln Xaa Leu His Asp Gln Ile Ala Gly Gln Lys Ala Ser Lys Gln Glu
 20 25 30
 10 Leu Glu Thr Glu Leu Glu Arg Leu Lys Gln Glu Phe His Tyr Ile Glu
 35 40 45
 Glu Asp Leu Tyr Arg Thr Lys Asn Thr Leu Gln Ser Arg Ile Lys Asp
 50 55 60
 15 Arg Asp Glu Glu Ile Gln Lys Leu Arg Asn Gln Leu Thr Asn Lys Thr
 65 70 75 80
 Leu Ser Asn Ser Ser Gln Ser Glu Leu Glu Asn Arg Leu His Gln Leu
 85 90 95
 Thr Glu Thr Leu Ile Gln Lys Gln Thr Met Leu Glu Ser Leu Ser Thr
 100 105 110
 25 Glu Lys Asn Ser Leu Val Phe Gln Leu Glu Arg Leu Glu Gln Gln Met
 115 120 125
 Asn Ser Ala Ser Gly Ser Ser Ser Asn Gly Ser Ser Ile Asn Met Ser
 130 135 140
 30 Gly Ile Asp Asn Gly Glu Gly Thr Arg Leu Arg Asn Val Pro Val Leu
 145 150 155 160
 Phe Asn Asp Thr Glu Thr Asn Leu Ala Gly Met Tyr Gly Lys Val Arg
 165 170 175
 Lys Ala Ala Ser Ser Ile Asp Gln Phe Ser Ile Arg Leu Gly Ile Phe
 180 185 190
 40 Leu Arg Arg Tyr Pro Ile Ala Arg Val Phe Val Ile Ile Tyr Met Ala
 195 200 205
 Leu Leu His Leu Trp Val Met Ile Val Leu Leu Thr Tyr Thr Pro Glu
 210 215 220
 45 Met His His Asp Gln Pro Tyr Gly Lys
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

60 Ile Arg His Glu Gln His Pro Asn Phe Ser Leu Glu Met His Ser Lys
 1 5 10 15

Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile Leu Ile Leu Pro
 20 25 30

5 Val Cys Ala His Leu His Glu Glu Leu Asn Cys
 35 40

10 (2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

Ser Phe Phe Ile Ser Glu Glu Lys Gly His Leu Leu Leu Gln Ala Glu
 1 5 10 15

20 Arg His Pro Trp Val Ala Gly Ala Leu Val Gly Val Ser Gly Gly Leu
 20 25 30

25 Thr Leu Thr Thr Cys Ser Gly Pro Thr Glu Lys Pro Ala Thr Lys Asn
 35 40 45

Tyr Phe Leu Lys Arg Leu Leu Gln Glu Met His Ile Arg Ala Asn
 50 55 60

30

35

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97897
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209043
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>119</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97898
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209044
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;"><div style="text-align: center;">For receiving Office use only</div></div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" style="margin-right: 10px;" type="checkbox"/><div>This sheet was received with the international application</div></div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;"><div style="text-align: center;">For International Bureau use only</div></div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input style="margin-right: 10px;" type="checkbox"/><div>This sheet was received by the International Bureau on:</div></div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97899
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209045
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White POT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97900</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <div><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div>Authorized officer <p style="text-align: center;">Susan White PCT International Division</p></div>	<p style="text-align: center;">For International Bureau use only</p> <div><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div>Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209046
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="display: flex; justify-content: space-between;"><div style="width: 40%;">Authorized officer</div><div style="width: 60%; text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="display: flex; justify-content: space-between;"><div style="width: 40%;">Authorized officer</div><div style="width: 60%;"></div></div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209047
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 22, 1997	Accession Number 209076
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>140</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 -- United States of America</p>	
Date of deposit <u>August 21, 1997</u>	Accession Number <u>209215</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97904
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit July 3, 1997	Accession Number 209139
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209049
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97903
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit June 12, 1997	Accession Number 209119
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97902
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209048
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209050
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer: <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer Susan White PCT International Division	Authorized officer

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
- 5
- (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - 10 (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
 - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
 - 20 (f) a polynucleotide which is a variant of SEQ ID NO:X;
 - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
 - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
 - (i) a polynucleotide capable of hybridizing under stringent conditions to any
 - 25 one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
- 30
3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
- 35

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
- 5
5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 10
6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 15
7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.
8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.
- 20
9. A recombinant host cell produced by the method of claim 8.
10. The recombinant host cell of claim 9 comprising vector sequences.
11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
- 25
- (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
 - 30 (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in
 - 35 ATCC Deposit No:Z;
 - (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

11. 14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:
 (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
 (b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

 17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

 (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
 (b) diagnosing a pathological condition or a susceptibility to a pathological
30 condition based on the presence or absence of said mutation.

 19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

35 (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ : C12N 15/12, 5/10, 1/21, C07K 14/47, 16/18, C12Q 1/68, G01N 33/50, 33/53; 33/68, A61K 38/17</p>	<p>A3</p>	<p>(11) International Publication Number: WO 98/39448</p> <p>(43) International Publication Date: 11 September 1998 (11.09.98)</p>																															
<p>(21) International Application Number: PCT/US98/04493</p> <p>(22) International Filing Date: 6 March 1998 (06.03.98)</p> <p>(30) Priority Data:</p> <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 30%;">60/040,162</td> <td style="width: 40%;">7 March 1997 (07.03.97)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/040,333</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/038,621</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/040,161</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/040,626</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/040,334</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/040,336</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/040,163</td> <td>7 March 1997 (07.03.97)</td> <td>US</td> </tr> <tr> <td>60/043,580</td> <td>11 April 1997 (11.04.97)</td> <td>US</td> </tr> <tr> <td>60/043,568</td> <td>11 April 1997 (11.04.97)</td> <td>US</td> </tr> </table> <p><i>(Continued on the following page)</i></p> <p>(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hills Road, Laytonsville, MD 20882 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield, Place, Centerville, VA 22020 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). BEDNARIK, Daniel, P. [US/US]; 8822 Blue Sea Drive, Columbia, MD 21046 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown,</p>			60/040,162	7 March 1997 (07.03.97)	US	60/040,333	7 March 1997 (07.03.97)	US	60/038,621	7 March 1997 (07.03.97)	US	60/040,161	7 March 1997 (07.03.97)	US	60/040,626	7 March 1997 (07.03.97)	US	60/040,334	7 March 1997 (07.03.97)	US	60/040,336	7 March 1997 (07.03.97)	US	60/040,163	7 March 1997 (07.03.97)	US	60/043,580	11 April 1997 (11.04.97)	US	60/043,568	11 April 1997 (11.04.97)	US	<p>MD 20874 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mount Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment #104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [BU/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US).</p> <p>(74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BI, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published</p> <p><i>With international search report.</i></p> <p><i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p> <p><i>With an indication in relation to deposited biological material furnished under Rule 13^{bis} separately from the description.</i></p> <p>(88) Date of publication of the international search report: 26 November 1998 (26.11.98)</p>
60/040,162	7 March 1997 (07.03.97)	US																															
60/040,333	7 March 1997 (07.03.97)	US																															
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60/043,580	11 April 1997 (11.04.97)	US																															
60/043,568	11 April 1997 (11.04.97)	US																															
<p>(54) Title: 186 HUMAN SECRETED PROTEINS</p> <p>(57) Abstract</p> <p>The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>																																	

60/043,314	11 april 1997 (11.04.97)	US	60/047,596	23 May 1997 (23.05.97)	US	60/056,637	22 August 1997 (22.08.97)	US
60/043,569	11 april 1997 (11.04.97)	US	60/047,612	23 May 1997 (23.05.97)	US	60/056,903	22 August 1997 (22.08.97)	US
60/043,311	11 april 1997 (11.04.97)	US	60/047,632	23 May 1997 (23.05.97)	US	60/056,888	22 August 1997 (22.08.97)	US
60/043,671	11 april 1997 (11.04.97)	US	60/047,601	23 May 1997 (23.05.97)	US	60/056,879	22 August 1997 (22.08.97)	US
60/043,674	11 april 1997 (11.04.97)	US	60/047,595	23 May 1997 (23.05.97)	US	60/056,880	22 August 1997 (22.08.97)	US
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60/043,312	11 april 1997 (11.04.97)	US	60/047,588	23 May 1997 (23.05.97)	US	60/056,911	22 August 1997 (22.08.97)	US
60/043,313	11 april 1997 (11.04.97)	US	60/047,585	23 May 1997 (23.05.97)	US	60/056,636	22 August 1997 (22.08.97)	US
60/043,672	11 april 1997 (11.04.97)	US	60/047,586	23 May 1997 (23.05.97)	US	60/056,874	22 August 1997 (22.08.97)	US
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60/047,615	23 May 1997 (23.05.97)	US	60/047,614	23 May 1997 (23.05.97)	US	60/056,892	22 August 1997 (22.08.97)	US
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60/047,633	23 May 1997 (23.05.97)	US	60/048,964	06 June 1997 (06.06.97)	US	60/056,876	22 August 1997 (22.08.97)	US
60/047,583	23 May 1997 (23.05.97)	US	60/049,610	13 June 1997 (13.06.97)	US	60/056,881	22 August 1997 (22.08.97)	US
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60/047,500	23 May 1997 (23.05.97)	US	60/056,893	22 August 1997 (22.08.97)	US	60/057,761	05 September 1997 (05.09.97)	US
60/047,587	23 May 1997 (23.05.97)	US	60/056,630	22 August 1997 (22.08.97)	US	60/057,650	05 September 1997 (05.09.97)	US
60/047,492	23 May 1997 (23.05.97)	US	60/056,878	22 August 1997 (22.08.97)	US	60/057,669	05 September 1997 (05.09.97)	US
60/047,598	23 May 1997 (23.05.97)	US	60/056,662	22 August 1997 (22.08.97)	US	60/058,785	12 September 1997 (12.09.97)	US
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INTERNATIONAL SEARCH REPORT

International Application No.

PCT, JS 98/04493

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6	C12N15/12	C12N5/10	C12N1/21	C07K14/47	C07K16/18
	C12Q1/68	G01N33/50	G01N33/53	G01N33/68	A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	L. HILLIER ET AL.: "The WashU-Merck EST Project" EMBL SEQUENCE DATABASE, 25 January 1996, HEIDELBERG, FRG, XP002068330 yy50d03.s1 Homo sapiens cDNA clone 276965 3'; Accession no. N39235;	1-3, 7-11,21
X	L. HILLIER ET AL.: "The WashU-Merck EST Project" EMBL SEQUENCE DATABASE, 3 July 1995, HEIDELBERG, FRG, XP002068331 ym24h05.s1 Homo sapiens cDNA clone 49109 3'; Accession no. H16400;	1-3, 7-11,21
	-/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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- "P" document published prior to the international filing date but later than the priority date claimed

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- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

28.09.98

Name and mailing address of the ISA

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HORNIG H.

INTERNATIONAL SEARCH REPORT

International Application No

PCT, JS 98/04493

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 679 716 A (MATSUBARA KENICHI ;OKUBO KOUSAKU (JP)) 2 November 1995 SEQ ID no.3616 see page 1144, line 10 - line 24; claims 1-6 ---	1-3, 7-10,21
A	WO 97 07198 A (GENETICS INSTITUT) 27 February 1997 see the whole document ---	1-23
A	WO 97 04097 A (GENETICS INST) 6 February 1997 see the whole document ---	1-23
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 see the whole document ---	1-23
A	JACOBS K ET AL: "A novel method for isolating eukaryotic cDNA clones encoding secreted proteins." KEYSTONE SYMPOSIUM ON DENDRITIC CELLS: ANTIGEN PRESENTING CELLS OF T AND B LYMPHOCYTES, TAOS, NEW MEXICO, USA, MARCH 10-16, 1995. JOURNAL OF CELLULAR BIOCHEMISTRY SUPPLEMENT 0 (21A). 1995. 19. ISSN: 0733-1959, XP002027246 abstract no. C1-207 see abstract ---	1-23
A	WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document ---	1-23
A	WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document -----	1-23

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 04493

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 17 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-23 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-23) partially

-An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group of SEQ ID nos. 11, 197; wherein said polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein encoding the sequence selected from the group of SEQ ID nos. 313, 499 or the polypeptide encoded by the cDNA sequence included in ATCC Deposit no: 97897/209043, which is hybridizable to SEQ ID nos.11 and/or 197; a recombinant vector comprising said isolated nucleic acid molecule; a method of making a recombinant host cell comprising said isolated nucleic acid molecule; a recombinant host cell comprising said vector; an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group of SEQ ID nos. 313, 499; an isolated antibody that binds specifically to said isolated polypeptides; a recombinant host cell that expresses said isolated polypeptides; a method of making said polypeptides; a method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of said polypeptides; a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject using said polynucleotides and/or polypeptide sequences; a method for identifying a binding partner to said polypeptides; a gene corresponding to the cDNA sequences of SEQ ID nos.11 and/or 197; a method for identifying an activity in a biological assay, by using the expression of SEQ ID no. 313 and/or 499;

Inventions 2 to 186. Claims: (1-23) partially

-Idem as subject 1 but limited to gene nos. 2 to 186 respectively cDNA clone sequences HBGBW52 to HFAMH74.
(Invention 2 is limited to SEQ ID nos.12,198,314 and 500;
Invention 3 is limited to SEQ ID nos.13,199,315 and 501;
.....; Invention 186 is limited to SEQ ID nos.196, 312, 498 and 614;)

INTERNATIONAL SEARCH REPORT

ti nation on patent family members

International Application No

PCT, .S 98/04493

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